

Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWIGYIYSGSTNPNPSL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR--SDG-YTLDNWGGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

RESULT 5

US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 2.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWIGYIYSGSTNPNPSL 61
Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWIGYIYSGSTNPNPSL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR--SDG-YTLDNWGGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

RESULT 6

US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA

APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:


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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.le-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSTLSLTCTVSGSIRSGGYWYRWIRQPGKLEWIGYIYHSGNTYINPFL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSTLSLTCTVSGSIRSGGYWYRWIRQPGKLEWIGYIYHSGNTYINPFL 65

QY 62 KSRVTMSVDTSKNHFSLSLSSVTAADTAVYYCARSD----GYTLDNWQGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGSYGGYYGMDVMQGGTTVTVSS 122

RESULT 9
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

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Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.le-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSTLSLTCTVSGSIRSGGYWYRWIRQPGKLEWIGYIYHSGNTYINPFL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSTLSLTCTVSGSIRSGGYWYRWIRQPGKLEWIGYIYHSGNTYINPFL 65

QY 62 KSRVTMSVDTSKNHFSLSLSSVTAADTAVYYCARSD----GYTLDNWQGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGSYGGYYGMDVMQGGTTVTVSS 122

RESULT 10
US-08-450-363-11
; Sequence 11, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:

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TISSUE TYPE: Hybridoma producing human antibody 1-3-1
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE: Hybridoma producing human antibody 1-3-1

IMMEDIATE SOURCE:

ORGANELLER:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-11

Query Match 80.8%; Score 496; DB 4; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.1e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 61

Db 6 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARDSD---GYTLNMGQGLTVTVSS 114

Db 66 KSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARGSGYGGYGGMDVWGGGTTTVTVSS 122

RESULT 11

US-09-800-729-145

; Sequence 145, Application US/09800729

; Patent No. 6605592

; GENERAL INFORMATION:

; APPLICANT: Ni et al.

; TITLE OF INVENTION: 32 Human secreted proteins

; FILE REFERENCE: P2044PI

; CURRENT APPLICATION NUMBER: US/09/800,729

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: PCT/US00/26013

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155,709

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: Patent in ver. 2.0

; SEQ ID NO 145

; LENGTH: 487

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-800-729-145

Query Match 80.1%; Score 492; DB 4; Length 487;

Best Local Similarity 78.9%; Pred. No. 1.4e-41;

Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 2;

QY 2 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 61

Db 25 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 84

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARDSD---GYTLNMGQGLTVTVSS 111
Db 85 KSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARGSGYGGYGGMDVWGGGTTTVTVSS 144

QY 112 VSS 114

Db 145 VSS 147

RESULT 12

US-09-025-769B-25

; Sequence 25, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MOREPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 118 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-025-769B-25

Query Match 80.0%; Score 491; DB 4; Length 118;

Best Local Similarity 84.3%; Pred. No. 3.2e-42;

Matches 97; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 61

Db 6 ESGPGLVKPSETLSLTCTVSGGSISSGGYYSWIRQPPGKGLWIGYIHSGNTYNPSSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARDSD---GYTLNMGQGLTVTVSS 114

Db 64 KSRVTISVDTSKNQFSLRLSSVTAADTAVYVCARGSGYGGYGGMDVWGGGTTTVTVSS 118

RESULT 13

US-08-360-125-5

; Sequence 5, Application US/08360125

; Patent No. 5767246

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 57672461hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
Query Match 79.4%; Score 487.5; DB 1; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
Qy 2 ESGPGLVKPSQTLSTCTVSGGSRSGYKWSWIRQPGKGLWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSRSGYKWSWIRQPGKGLWIGYIYHSGNTYYNPSL 65
Qy 62 KSRVTMSVDTSKNHFSRLSSVTAADTAVYVCARSDGYT-LDNWGQGTFLTVSS 114
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYVCARSTRLRGADYWGQGTFLTVSS 119
RESULT 14
US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
US-08-450-578-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWIRQPPGKGLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWIRQPPGKGLEWIGYIYHSGNTYINPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAAATVYYCARSDGYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKQFSLKLSLTAADTAVYYCARSTRRLRGADYWGQGTMTVTVSS 119

Search completed: August 8, 2004, 12:20:24
Job time : 13.6455 secs

; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWIRQPPGKGLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWIRQPPGKGLEWIGYIYHSGNTYINPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAAATVYYCARSDGYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKQFSLKLSLTAADTAVYYCARSTRRLRGADYWGQGTMTVTVSS 119

RESULT 15
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 9 31515 Seconds
(without alignments)
1094.593 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASVTFGGTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	85.5	127	2 S40367	Ig kappa chain V-J
2	459	84.5	123	2 S40331	Ig kappa chain - h
3	458	84.3	108	2 S49047	Ig kappa chain V r
4	456	84.0	108	2 S47182	Ig kappa chain - h
5	452	83.2	109	2 S31979	Ig kappa chain - h
6	452	83.2	109	2 S31980	Ig kappa chain - h
7	448	82.5	109	2 S31980	Ig kappa chain - h
8	445	82.1	108	2 S44122	Ig kappa chain V r
9	445	82.0	109	2 S32001	Ig kappa chain - h
10	441	81.2	108	2 S19674	Ig kappa chain V r
11	439	80.8	109	2 S31981	Ig kappa chain - h
12	439	80.8	129	2 S52793	Ig kappa chain V r
13	438	80.7	107	2 S36264	Ig kappa chain V r
14	437	80.5	108	2 S31977	Ig kappa chain - h
15	436	80.3	109	2 S31983	Ig kappa chain - h
16	436	80.3	122	2 S40370	Ig kappa chain - h
17	436	80.3	129	1 K1HUWK	Ig kappa chain pre
18	436	80.3	129	2 S40317	Ig kappa chain - h
19	435	80.1	128	2 S46372	Ig kappa chain V-J
20	434	79.9	120	2 S46370	Ig kappa chain - h
21	433.5	79.8	125	2 S40315	Ig kappa chain - h
22	433	79.7	128	1 K1HUDE	Ig kappa chain V-I
23	432	79.6	132	2 S40334	Ig kappa chain - h
24	431	79.4	109	2 S31978	Ig kappa chain - h
25	430	79.2	108	1 K1HUHU	Ig kappa chain V-I
26	430	79.2	132	2 S38646	Ig kappa chain V r
27	425	78.3	122	2 S40314	Ig kappa chain - h
28	425	78.3	129	2 S40369	Ig kappa chain - h
29	424.5	78.2	106	2 PC2397	anti-tetanus toxin

30	423.5	78.0	124	2 S40336	Ig kappa chain V-J
31	422.5	77.8	107	2 S36275	Ig lambda chain V
32	422	77.7	125	2 S40333	Ig kappa chain V-J
33	422	77.7	131	2 S40352	Ig kappa chain V-J
34	420	77.3	108	1 K1HUOU	Ig kappa chain V-I
35	420	77.3	125	2 S40349	Ig kappa chain V-J
36	420	77.3	126	2 S40335	Ig kappa chain V-J
37	419	77.2	125	2 S40350	Ig kappa chain V-J
38	418	77.0	117	2 S46371	Ig kappa chain - h
39	418	77.0	129	2 S52792	Ig kappa chain V-J
40	417	76.8	117	2 S46376	Ig kappa chain V-J
41	416	76.6	108	1 K1HUEU	Ig kappa chain V-I
42	414	76.2	107	2 JLD139	Ig kappa chain V-I
43	414	76.2	107	2 S36262	Ig kappa chain V r
44	414	76.2	108	1 K1HUKA	Ig kappa chain V-I
45	413.5	76.2	108	2 S30521	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40367
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;
Best Local Similarity 84.9%; Pred. No. 4e-36;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy	1	ELTQSPSSLSASVGDRTVISCRASQRIINTYLNHYQHFKGKAPKLLIYAASSLSQSGVPSRF	60
Db	20	QMTQSPSSLSASVGDRTVITCRASQISINLYNWKPKGKAPKLLIYAASSLSQSGVPSRF	79
Qy	61	SGSGYGTDFLTITISSLOFEDFASYSQESLSASVTFGGTKVEIKR	106
Db	80	SGSGSGTDFLTITISSLQPEDFATYCCQSYNTPTWTFGGTKVEIKR	125

RESULT 2

S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40331
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 123;

Best Local Similarity 85.7%; Pred. No. 1.1e-35;
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Db 19 QMTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 78

QY 61 SGSGYGTDTLTITSSQLQPEDFATYYCQSSLSASYTFQGGTKVEIK 105

Db 79 SGSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTKVEIK 123

RESULT 3

B49047 Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm

A:Species: Homo sapiens (man)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B49047

R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes

A:Reference number: A49047; PMID:92387224; PMID:1516616

A:Accession: B49047

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-108 <VIC>

A:Experimental source: thymic B lymphocytes

A>Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;

Best Local Similarity 84.9%; Pred. No. 1.2e-35;

Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Db 3 QMTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDTLTITSSQLQPEDFATYYCQSSLSASYTFQGGTKVEIK 106

Db 63 SGSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTKVEIK 108

RESULT 4

S47182 Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S47182

R:McIntosh, R.S.; Randon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL data library, June 1994

A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient

A:Reference number: S47181

A:Accession: S47182

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <MC1>

A:Cross-references: EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PID:G506423

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;

Best Local Similarity 84.9%; Pred. No. 1.8e-35;

Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Db 3 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDTLTITSSQLQPEDFATYYCQSSLSASYTFQGGTKVEIK 106

Db 63 SGSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTKVEIK 108

Db 63 SGSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTRLEIKR 108

RESULT 5

S31979 Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31979

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL data library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations

A:Reference number: S31977

A:Accession: S31979

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID:G38490

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;

Best Local Similarity 81.9%; Pred. No. 4.4e-35;

Matches 86; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

Db 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSQLQPEDFATYYCQSSLSASYTFQGGTKVEIKR 106

Db 64 GSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTRLEIKR 108

RESULT 6

S31998 Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C:Accession: S31998

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL data library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations

A:Reference number: S31977

A:Accession: S31998

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;

Best Local Similarity 83.8%; Pred. No. 4.4e-35;

Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

Db 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSQLQPEDFATYYCQSSLSASYTFQGGTKVEIKR 106

Db 64 GSGGTDTLTITSSQLQPEDFATYYCQSSYSTPTFTFGGTRLEIKR 108

RESULT 7

S31980 Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31980; S32000

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 5.78192 Seconds
(without alignments)
954.620 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGRVTIS.....QESLSASVTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	436	80.3	129	1 KVI4A_HUMAN	P04431 homo sapien
2	433	79.7	108	1 KVI1I_HUMAN	P01597 homo sapien
3	430	79.2	108	1 KVIH_HUMAN	P01600 homo sapien
4	420	77.3	108	1 KVIN_HUMAN	P01606 homo sapien
5	416	76.6	108	1 KVI1F_HUMAN	P01598 homo sapien
6	414	76.2	108	1 KVIK_HUMAN	P01603 homo sapien
7	413	76.1	108	1 KVI4V_HUMAN	P04430 homo sapien
8	412	75.9	108	1 KVI1O_HUMAN	P01607 homo sapien
9	409	75.3	108	1 KVI1G_HUMAN	P01599 homo sapien
10	408	75.1	108	1 KVI1B_HUMAN	P01605 homo sapien
11	407	75.0	108	1 KVI1M_HUMAN	P01594 homo sapien
12	406	74.8	108	1 KVI1R_HUMAN	P01610 homo sapien
13	404	74.4	108	1 KVI1A_HUMAN	P01593 homo sapien
14	399.5	73.6	107	1 KVID_HUMAN	P01596 homo sapien
15	399	73.5	108	1 KVI1S_HUMAN	P01611 homo sapien
16	398	73.3	108	1 KVI1P_HUMAN	P01608 homo sapien
17	397	73.1	108	1 KVI1L_HUMAN	P01604 homo sapien
18	397	73.1	129	1 KVI1X_HUMAN	P04432 homo sapien
19	396	72.9	108	1 KVI1Y_HUMAN	P03062 homo sapien
20	391	72.0	108	1 KVI1Q_HUMAN	P01609 homo sapien
21	385.5	71.0	109	1 KVI1T_HUMAN	P01612 homo sapien
22	384	70.7	108	1 KVI1C_HUMAN	P01595 homo sapien
23	376	69.2	108	1 KVI5T_MOUSE	P01653 mus musculus
24	373	68.7	108	1 KVI5S_MOUSE	P01652 mus musculus
25	370.5	68.2	109	1 KVI3E_HUMAN	P01623 homo sapien
26	370	68.1	108	1 KVI5Q_MOUSE	P01650 mus musculus
27	368.5	67.9	109	1 KVI3B_HUMAN	P01620 homo sapien
28	368.5	67.9	109	1 KVI3D_HUMAN	P01622 homo sapien
29	368	67.8	108	1 KVI5N_MOUSE	P01647 mus musculus
30	368	67.8	108	1 KVI5O_MOUSE	P01648 mus musculus
31	368	67.8	117	1 KVI1J_HUMAN	P01602 homo sapien
32	367.5	67.7	129	1 KVI3M_HUMAN	P18136 homo sapien
33	366.5	67.5	129	1 KVI3L_HUMAN	P18135 homo sapien

34	366	67.4	114	1 KVI4A_HUMAN	P01625 homo sapien
35	366	67.4	117	1 KVI1I_HUMAN	P01601 homo sapien
36	365	67.2	108	1 KVI5K_MOUSE	P01644 mus musculus
37	365	67.2	108	1 KVI5M_MOUSE	P01646 mus musculus
38	365	67.2	134	1 KVI4C_HUMAN	P06314 homo sapien
39	364	67.0	108	1 KVI5R_MOUSE	P01651 mus musculus
40	363	66.9	111	1 KVI3M_MOUSE	P01665 mus musculus
41	362	66.7	111	1 KVI3L_MOUSE	P01664 mus musculus
42	361	66.5	108	1 KVI5P_MOUSE	P01649 mus musculus
43	360	66.3	108	1 KVI5L_MOUSE	P01645 mus musculus
44	358	65.9	111	1 KVI3O_MOUSE	P01667 mus musculus
45	357	65.7	128	1 KVI5E_MOUSE	P01637 mus musculus

ALIGNMENTS

RESULT 1

KVI4V_HUMAN
ID KVI4V_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL; X00965; CAA25477.1; ALT_TERM.
PIR; A01883; K1HUWK.
HSSP; P01607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 22
CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 119 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 80.3%; Score 436; DB 1; Length 129;
Best Local Similarity 81.9%; Pred. No. 8,2e-40;
Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHCKAPKLLIYAASSLSQSGVPSRF 60
 DB 25 QMTQSPSSLSASVGRVTITTCRASQISNLYNWKQKPGKAPKLLIYAASSLSQSGVTSRF 84

QY 61 SSGSGYGTDFTLTISLQFEDFASYCQESLSASYTFQGQTKVEIK 105
 DB 85 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFQGQTRLEIK 129

RESULT 2

KVIN HUMAN STANDARD; PRT; 108 AA.
 ID KVIN HUMAN STANDARD; PRT; 108 AA.
 AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P.; Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain."
 RL Biochem. J. 123:945-958(1971).
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin v region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
 Best Local Similarity 77.4%; Pred. No. 1.4e-39;
 Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHCKAPKLLIYAASSLSQSGVPSRF 60
 DB 3 ZMTQSPSSLSASVGRVTITTCRASQSVNLYNWKQKPGKAPKLLIYAASSLSQSGVPSRF 62
 QY 61 SSGSGYGTDFTLTISLQFEDFASYCQESLSASYTFQGQTKVEIK 106
 DB 63 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFQGQTKVEMTR 108

RESULT 3

KVIN HUMAN STANDARD; PRT; 108 AA.
 ID KVIN HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S.; Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01868; KIHURU.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin v region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 3e-39;
 Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHCKAPKLLIYAASSLSQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGRVTITTCRASQISNLYNWKQKPGKAPKLLIYAASSLSQSGVPSRF 62
 QY 61 SSGSGYGTDFTLTISLQFEDFASYCQESLSASYTFQGQTKVEIK 106
 DB 63 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFQGQTRVEIKR 108

RESULT 4

KVIN HUMAN STANDARD; PRT; 108 AA.
 ID KVIN HUMAN STANDARD; PRT; 108 AA.
 AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H.; Shimizu A.; Paul C.; Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy chains."
 RL Science 169:56-59(1970).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM S MACROGLOBULIN.
 DR PIR; A01872; KIHUOU.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.


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DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 108 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA4A24105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 3.5e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPSTLSASVGDRTVITCRASQITSSYLEWYZZKFGKAPBLIIYAASLHSGVPSRF 62

QY 61 SSGSGVTDFTLTISLQPEDFASYVCQESLSASVTFGGQTKVEIKR 106
Db 63 SSGSGTBTFTTISLZPZBFATYTCZZSYSPPTFGZGTRLZIKR 108

RESULT 5
KVLF_HUMAN
ID KVLF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. V. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHUEU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 108 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA4A24105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 3.5e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPSTLSASVGDRTVITCRASQITSSYLEWYZZKFGKAPBLIIYAASLHSGVPSRF 62

QY 61 SSGSGVTDFTLTISLQPEDFASYVCQESLSASVTFGGQTKVEIKR 106
Db 63 SSGSGTBTFTTISLZPZBFATYTCZZSYSPPTFGZGTRLZIKR 108
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FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 9.3e-38;
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPSTLSASVGDRTVITCRASQITSSYLEWYZZKFGKAPBLIIYAASLHSGVPSRF 62

QY 61 SSGSGVTDFTLTISLQPEDFASYVCQESLSASVTFGGQTKVEIK 105
Db 63 IGSQSGTEFTLTISLQPDFFATYCYQYNSDSKMFQGGTKVEVK 107

RESULT 6
KVLF_HUMAN
ID KVLF_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; IMTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1.5e-37;
Matches 75; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPSTLSASVGDRTVITCRASQITSSYLEWYZZKFGKAPBLIIYAASLHSGVPSRF 62
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OY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGGQTKVIEKR 106
DB 63 SQGSGTBTFTTSSVZPZBFAIYYCQZYLDLPRFGQTKVDLKR 108

RESULT 7
KVIV_HUMAN STANDARD; PRT; 108 AA.
AC F04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR HSP; P80362; L1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 76.1%; Score 413; DB 1; Length 108;
Best Local Similarity 76.4%; Pred. No. 2e-37;
Matches 81; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 3 QLTQSPSSLSASVGDRTVITSCRASQSVYVNVAFQKPGKAPKSLIYDASTLSQGVPSNF 62

OY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGGQTKVIEKR 106
DB 63 TGSQSGTDFLTITSSLOPEDFATYYCQVNSYPTFTGGQTKVQIKR 108

RESULT 8
KVIO_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=76023758; PubMed=809329;
RX

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RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Re1); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein RE1 refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWW; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 75.9%; Score 412; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 2.5e-37;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITSCASQDI IKYLNWYQTPGKAPKLLIYASNLQGVPSRF 62

OY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGGQTKVIEKR 106
DB 63 SSGSGTDFLTITSSLOPEDIATYYCQYQSLPYTFGGQTKLQITR 108

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RESULT 9
KVIG_HUMAN
ID   KVIG_HUMAN          STANDARD;          PRT;   108 AA.
AC   P01599;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Gal.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059122; PubMed=4215718;
RA   Laure C.-J., Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), 1. The amino acid sequence of the L-chain of
RL   kappa-type, subgroup I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC   CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC   MACROGLOBULIN.
DR   PIR; A01867; KIHUGL.
DR   HSP; P01607; IREI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1 23
FT   DOMAIN 24 34
FT   DOMAIN 35 49
FT   DOMAIN 50 56
FT   DOMAIN 57 88
FT   DOMAIN 89 97
FT   DOMAIN 98 107
FT   DISULFID 23 88
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11914 MW; 13AD3CB0F600FF73 CRC64;
      FRAMEWORK-1.
      COMPLEMENTARITY-DETERMINING-1.
      FRAMEWORK-2.
      COMPLEMENTARITY-DETERMINING-2.
      FRAMEWORK-3.
      COMPLEMENTARITY-DETERMINING-3.
      FRAMEWORK-4.
      BY SIMILARITY.

Query Match      75.3%; Score 409; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 5.3e-37;
Matches 83; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSLASASVGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLQSGVPSRF 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 QMTQSPSLASASVGDRVTIICRASQGIKNDLTWYQKPGKAPKLLIYAASNLQSGVPSRF 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 SGTSGYGTDFLTITSSLOFEPASVYQCESLSASVTFGGTKVEIKR 106
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 SGTSGAGTEFTLTSSLOPEDFATYICLQNSYPSRFGSGTKVEIKR 108
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
KVIM_HUMAN
ID   KVIM_HUMAN          STANDARD;          PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.

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RL Biophys. Struct. Mech. 1:139-146 (1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91653; KIHUAG.
DR PDB; 1UV5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6B9 CRC64;

Query Match 75.0%; Score 407; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 8.6e-37;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 3 QMTQSPSSLSASVGRVTITCRASQIRNLTWYQKPGKAPKLLIYDASNLSQSGVPSRF 62
QY 61 SSGSGYGTFTLTISLQPEDFASYCQESLSASYTFGQGTKEIKR 106
DB 63 SGGSGGAHTFTLTISLQPEDATYTCQYDYLPWTFGQGTKEIKR 108

RESULT 12
KVLR_HUMAN STANDARD; PRT; 108 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F.; Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 74.8%; Score 406; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 1.1e-36;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 3 QMTQSPSSLSASVGRVTITCRASQIRNLTWYQKPGKAPKLLIYGATSLQSGVPSRF 62
QY 61 SSGSGYGTFTLTISLQPEDFASYCQESLSASYTFGQGTKEIKR 106
DB 63 SGGSGGTFTLTINSLOPEDFATYCYCQYSSPFWTFGQGTKEIKR 108

RESULT 13
KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K.; Shinoda T.; Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560 (1969).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 74.4%; Score 404; DB 1; Length 108;
Best Local Similarity 73.6%; Pred. No. 1.8e-36;
Matches 78; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
```


GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 29.0697 Seconds
(without alignments)
1150.508 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDVRTVIS.....QESLSASTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	465	85.6	108	Q9UL77	Q9UL77 homo sapien
2	449.5	82.8	107	Q96SA9	Q96SA9 homo sapien
3	439.5	80.9	107	Q9UL81	Q9UL81 homo sapien
4	422	77.7	108	Q9UL79	Q9UL79 homo sapien
5	420	77.3	108	Q9UL70	Q9UL70 homo sapien
6	418	77.0	234	Q7Z473	Q7Z473 homo sapien
7	412	75.9	236	Q7Z3Y4	Q7Z3Y4 homo sapien
8	371	68.3	108	Q9UL83	Q9UL83 homo sapien
9	371	68.3	116	Q96PF6	Q96PF6 homo sapien
10	366	67.4	298	11 Q9QVF0	Q9QVF0 mus musculus
11	364	67.0	214	11 Q9RIA5	Q9RIA5 mus musculus
12	361	66.5	234	11 Q91WF8	Q91WF8 mus musculus
13	361	66.5	234	11 Q8R062	Q8R062 mus musculus
14	361	66.5	236	11 Q7TWK3	Q7TWK3 mus musculus
15	359	66.1	109	11 Q920E6	Q920E6 mus musculus
16	359	66.1	111	11 Q920E9	Q920E9 mus musculus

17	357	65.7	233	11 Q91WS9	Q91WS9 mus musculus
18	357	65.7	234	11 Q8VCP0	Q8VCP0 mus musculus
19	355.5	65.5	109	4 Q9UL78	Q9UL78 homo sapien
20	354	65.2	236	11 Q7TS98	Q7TS98 mus musculus
21	350	64.5	111	11 Q811U6	Q811U6 mus musculus
22	346.5	63.8	109	4 Q9UL86	Q9UL86 homo sapien
23	346	63.7	108	11 Q8V1D0	Q8V1D0 mus musculus
24	345.5	63.6	109	4 Q9UL85	Q9UL85 homo sapien
25	335.5	61.8	243	11 Q7TQM2	Q7TQM2 mus musculus
26	332.5	61.2	112	11 Q8K1F3	Q8K1F3 mus musculus
27	332.5	61.2	235	11 Q7TMK0	Q7TMK0 mus musculus
28	332	61.1	107	11 Q9ER29	Q9ER29 mus musculus
29	330.5	60.9	238	11 Q99M37	Q99M37 mus musculus
30	329.5	60.7	114	11 Q8K1F1	Q8K1F1 mus musculus
31	328	60.4	127	11 Q925S9	Q925S9 mus musculus
32	328	60.4	131	11 Q811C3	Q811C3 mus musculus
33	325.5	59.9	112	11 Q8K1F2	Q8K1F2 mus musculus
34	323	59.5	99	11 Q9JL74	Q9JL74 mus musculus
35	321.5	59.2	238	11 Q8VC16	Q8VC16 mus musculus
36	320.5	59.0	134	11 Q8VDD0	Q8VDD0 mus musculus
37	320.5	59.0	241	11 Q921A6	Q921A6 mus musculus
38	319	58.7	107	11 Q9JL84	Q9JL84 mus musculus
39	317	58.4	237	13 Q7SZ36	Q7SZ36 xenopus lae
40	315	58.0	103	11 Q9JL80	Q9JL80 mus musculus
41	314.5	57.9	239	4 Q8NEK0	Q8NEK0 homo sapien
42	311.5	57.4	106	5 Q9U410	Q9U410 schistosoma
43	308	56.7	234	11 Q8R028	Q8R028 mus musculus
44	307.5	56.6	239	11 Q8VC55	Q8VC55 mus musculus
45	305.5	56.3	104	11 Q9JL82	Q9JL82 mus musculus

ALIGNMENTS

RESULT 1

Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 85.6%; Score 465; DB 4; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.7e-44;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVRTVISCRASQRIINTYQHKAPKLLIYAASSLOSQGVPSRF 60

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:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPNLLIYAASSLQSGVPSRF 62

Db
QY 61 SSGSGYGTDTLTISLQFEDFASYCYQESLSASVTFQGTKEIKR 106
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
63 SSGSGGTDTLTISLQFEDFATYCYQSQSYSTSWTFEGTKVEIKR 108

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 82.8%; Score 449.5; DB 4; Length 107;
Best Local Similarity 84.9%; Pred. No. 9.1e-43;
Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPKAPKLLIYAASSLQSGVPSRF 60
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKLLIYAASSLQSGVPSRF 62

QY 61 SSGSGYGTDTLTISLQFEDFASYCYQESLSASVTFQGTKEIKR 106
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
63 SSGSGGTDTLTISLQFEDFATYCYQSQSYSTSWTFEGTKVEIKR 107

RESULT 3
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPKAPKLLIYAASSLQSGVPSRF 61
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
4 MTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQKPKAPKLLIYAASSLQSGVPSRF 63

QY 62 GSGYGTDTLTISLQFEDFASYCYQESLSASVTFQGTKEIKR 106
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
64 GSGSGTDTLTISLQFEDFATYCYQSQSYSTSWTFEGTKVEIKR 108

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"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.9%; Score 439.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.2e-41;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPKAPKLLIYAASSLQSGVPSRF 60
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPNLLIYAASSLQSGVPSRF 62

QY 61 SSGSGYGTDTLTISLQFEDFASYCYQESLSASVTFQGTKEIKR 106
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
63 SSGSGTDTLTISLQFEDFATYCYQSQSYSTSWTFEGTKVEIKR 107

RESULT 4
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPKAPKLLIYAASSLQSGVPSRF 61
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
4 MTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQKPKAPKLLIYAASSLQSGVPSRF 63

QY 62 GSGYGTDTLTISLQFEDFASYCYQESLSASVTFQGTKEIKR 106
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
64 GSGSGTDTLTISLQFEDFATYCYQSQSYSTSWTFEGTKVEIKR 108

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QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 ELTQSPSSLSASVGVETVITCRAGNIHNYLAWIQKQKGSQPLLNVNAKTLADGVPSRF 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCQESLSASYTFGGQTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 SSGSGGQYSLKINSLOPEDFGSYCYQHFWTPTTFGGGTKLEIKR 280
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
Q91WF8 Q91AF5 PRELIMINARY; PRT; 214 AA.
AC Q91AF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -
DR PDB; 1C1C; 11-MAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K60; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 67.0%; Score 364; DB 11; Length 214;
Best Local Similarity 64.2%; Pred. No. 9.le-33;
Matches 68; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QLTQSPSSMYASLGERVTITCKASQDINSYLSWQFQKRGKSPKLLIYRANLVDGVPSRF 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCQESLSASYTFGGQTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGQYSLTISSEYEDMGVIYCIQYDFEFTFGSGTKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
Q91WF8 Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 2.2e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTSSLSASLGDRVTISCRASQGISYLNWYQKPDGTVKLLIYTSLSHSGVPSRF 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCQESLSASYTFGGQTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQYQSFPTFGSGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAHL5292.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; E0D0B0E6EB7812D2 CRC64;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 2.2e-32;
Matches 69; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTSSLSASLGDRVTISCRASQDISYLNWYQKPDGTVKLLIYTSLSHSGVPSRF 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCQESLSASYTFGGQTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQYQSFPTFGSGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 13
Q9R062 Q9R062 PRELIMINARY; PRT; 234 AA.
AC Q9R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 2.2e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTSSLSASLGDRVTISCRASQGISYLNWYQKPDGTVKLLIYTSLSHSGVPSRF 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCQESLSASYTFGGQTKVEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQYQSFPTFGSGTKLEIKR 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 14

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 43 5242 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFQGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	533	98.2	106	5	ABG30448 Human IgE
2	475	87.5	107	2	AAR54260 Anti-HIV
3	475	87.5	107	2	AAW01283 VL region
4	475	87.5	107	3	AAW98244 Anti-gp12
5	475	87.5	107	3	AAW95135 Anti-gp12
6	474	87.3	107	4	AAG93667 Human ant
7	474	87.3	107	6	ABO27474 Anti-Rh(D
8	472	86.9	107	4	AAG93663 Human ant
9	472	86.9	107	4	AAG93664 Human ant
10	472	86.9	107	4	AAG93590 Human ant
11	472	86.9	107	6	ABO27471 Anti-Rh(D
12	472	86.9	107	6	ABO27397 Anti-Rh(D
13	472	86.9	107	6	ABO27470 Anti-Rh(D
14	471	86.7	107	4	AAG93644 Human ant
15	471	86.7	107	6	ABO27451 Anti-Rh(D
16	468	86.2	107	4	AAG93593 Human ant
17	468	86.2	107	6	ABO27400 Anti-Rh(D
18	467	86.0	107	2	AAR54261 Anti-HIV
19	467	86.0	107	2	AAW01284 VL region
20	467	86.0	107	3	AAW98245 Anti-gp12
21	467	86.0	107	3	AAW95136 Anti-gp12
22	467	86.0	114	2	AAW13922 Light cha
23	465	85.6	111	4	AAG63656 Amino aci
24	465	85.6	111	6	ABJ38615 Hepatitis
25	465	85.6	132	2	AAW22842 Human ant

26	465	85.6	240	6	ABJ38595	Hepatitis
27	465	85.6	299	4	AAG63660	Amino aci
28	464.5	85.5	108	4	AAG93589	Human ant
29	464.5	85.5	108	4	AAG93600	Human ant
30	464.5	85.5	108	6	ABO27407	Anti-Rh(D
31	464.5	85.5	108	6	ABO27396	Anti-Rh(D
32	464	85.5	107	4	AAG93594	Human ant
33	464	85.5	107	6	ABO27401	Anti-Rh(D
34	464	85.5	108	6	ABP96009	HSA antib
35	464	85.5	240	2	AAAY02472	A single
36	464	85.5	240	4	AAAB46007	Human MUC
37	464	85.5	240	4	AAAB46038	Human TF
38	464	85.5	240	4	AAAB46008	Human MUC
39	464	85.5	240	4	AAAB46006	Human MUC
40	464	85.5	240	4	AAAB46005	Human MUC
41	464	85.5	240	6	ABP95997	Human Ser
42	462	85.1	107	4	AAG93596	Human ant
43	462	85.1	107	4	AAG93595	Human ant
44	462	85.1	107	6	ABO27403	Anti-Rh(D
45	462	85.1	107	6	ABO27402	Anti-Rh(D

ALIGNMENTS

RESULT 1
ABG30448
ID ABG30448 standard; protein; 106 AA.
XX AC ABG30448;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 94 light chain protein.
XX
KW Human; fab; anti-allergic; vaccine; grass pollen; phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21 /note= "FR1 region"
FT Region 22..32 /note= "CDR1 region"
FT Region 33..47 /note= "FR2 region"
FT Region 48..54 /note= "CDR2 protein"
FT Region 55..86 /note= "FR3 region"
FT Region 87..95 /note= "CDR2 region"
FT Region 96..104 /note= "FR4 region"
XX WO200253595-A1.
XX 11-JUL-2002.
XX 27-DEC-2001; 2001WO-SE002908.
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89640.
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 39; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC fab, clone 94 light chain protein of the invention
XX
SQ Sequence 106 AA;
Query Match 98.2%; Score 533; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 3.5e-33; Mismatches 1; Indels 0; Gaps 0;
Matches 105; Conservative 0;
QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
QY 61 SGSGYGTDTLTITISSLOPDPFASYCQESLSASYTFGQGTKEIKR 106
DB 61 SGSGYGTDTLTITISSLOPDPFASYCQESLSASYTFGQGTKEIKR 106
RESULT 2
AAR54260
ID AAR54260 standard; protein; 107 AA.
XX
AC AAR54260;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
DE
XX
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key
FT Region 1. .21 Location/Qualifiers
FT /label= FR1
FT Region 22. .33
FT /label= CDR1
FT Region 34. .48
FT /label= FR2
FT Region 49. .55
FT /label= CDR2
FT Region 56. .87
FT /label= FR3
FT Region 88. .95
FT /label= CDR3
FT Region 96. .107
FT /label= FR4
XX
PN WO9407922-A1.
XX
PD 14-APR-1994.
XX

PF 30-SEP-1993; 93WO-US009328.
XX
FR 30-SEP-1992; 92US-00954148.
XX
FA (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
PS Claim 5; Page 189; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XLI Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAB regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54260
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 107 AA;
Query Match 87.5%; Score 475; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.5e-29; Mismatches 7; Indels 0; Gaps 0;
Matches 93; Conservative 6;
QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 1 ELTQSPSSLASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
QY 61 SGSGYGTDTLTITISSLOPDPFASYCQESLSASYTFGQGTKEIKR 106
DB 61 SGSGYGTDTLTITISSLOPDPFATYYCQSQSYSTPTTFGQGTKEIKR 106
RESULT 3
AAW01283
ID AAW01283 standard; protein; 107 AA.
XX
AC AAW01283;
XX
DT 29-JAN-1997 (first entry)
XX
DE VL region of HIV neutralising MAb, clone b22 and B35.
XX
KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key
FT Region 1. .21 Location/Qualifiers
FT /label= FR1
FT Region 22. .32
FT /label= CDR1
FT Region 33. .47
FT /label= FR2
FT Region 48. .54
FT /label= CDR2
FT Region 55. .86
FT /label= FR3
FT Region 87. .95
FT /label= CDR3
FT Region 96. .107
FT /label= FR4
XX
PN
PD
XX

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PN WO9602273-A1.
XX 01-FEB-1996.
XX 11-JUL-1995; 95WO-US008743.
XX 18-JUL-1994; 94US-00276852.
XX (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
XX immuno:therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.
XX
XX The sequences given in AAW01261-92 represent the light chain variable
XX regions (VL) of a series of monoclonal antibodies (Mab's) which are
XX immunoreactive with HIV glycoprotein gp120 and are capable of
XX neutralising HIV. This sequence represents the sequence of the JK2 gene
XX clones, B22 and B35. A Mab containing this VL sequence has the capacity
XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by
XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds
XX mature gp120 preferentially over the precursor gp160. The Mab may be used
XX for determining immunocompetence of a human anti-HIV antibody and in the
XX detection of HIV infection
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 2; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
XX Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWQHKGKAPKLLIYAASLSQSGVPSRF 60
XX Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKFGKAPKLLIYAASLSQSGVPSRF 60
XX
XX Qy 61 SGSGYGTDFTLTISSLPQEDFASYCQESLSASVTFGQGTKEIKR 106
XX Db 61 SGSGSGTDFTLTISSLPQEDFATYCCQSYSTPTPTFGQGTKEIKR 106
XX
XX RESULT 4
XX AAY98244
XX ID AAY98244 standard; protein; 107 AA.
XX AC AAY98244;
XX XX
XX DT 04-JUL-2000 (first entry)
XX
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX
XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX KW passive immunotherapy; reduce severity; HIV-induced disease;
XX KW immunocompetence; active immunisation.
XX
XX OS Homo sapiens.
XX
XX PN AU9948754-A.
XX
XX PD 17-FEB-2000.
XX
XX PF 16-SEP-1999; 99AU-00048754.
XX
XX PR 16-SEP-1999; 99AU-00048754.
XX
XX PA (SCRI ) SCRIPPS RES INST.
XX
XX PI Burton DR, Barbas CF, Lerner RA;

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XX WPI; 2000-246867/22.
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AAY98206) and a
XX second polynucleotide encoding a light chain immunoglobulin amino acid
XX sequence; (b) inserting the first and second polynucleotide sequences
XX into a host cell; (c) maintaining the host cell in conditions which allow
XX the amino acid sequences encoded by the polynucleotides to be expressed
XX in the host cell; and (d) isolating the antibody comprising the heavy and
XX light chain immunoglobulin amino acid sequences from the host cell. The
XX anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used for
XX neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting HIV
XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the antibodies
XX associated with monoclonal antibodies of xenogeneic or chimeric
XX derivation
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 3; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
XX Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWQHKGKAPKLLIYAASLSQSGVPSRF 60
XX Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKFGKAPKLLIYAASLSQSGVPSRF 60
XX
XX Qy 61 SGSGYGTDFTLTISSLPQEDFASYCQESLSASVTFGQGTKEIKR 106
XX Db 61 SGSGSGTDFTLTISSLPQEDFATYCCQSYSTPTPTFGQGTKEIKR 106
XX
XX RESULT 5
XX AAY95135
XX ID AAY95135 standard; protein; 107 AA.
XX AC AAY95135;
XX XX
XX DT 30-JUN-2000 (first entry)
XX
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX
XX KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
XX OS Homo sapiens.
XX
XX PN AU9948756-A.

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XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX (SRI ) SCRIPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-293393/26.
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX
XX Example 9; Fig 11; 366pp; English.
XX
XX The present sequence represents a fragment of an anti-human
XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an
XX in vitro virus infectivity assay by 50%, at a concentration of less than
XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and
XX immunotherapy of HIV induced disease. They are useful as neutralising
XX field isolates and provide useful information regarding the
XX immunocompetence of an immune response in HIV infected patients. The
XX monoclonal antibodies are useful for producing anti-idiotypic antibodies
XX which can be used to screen human monoclonal antibodies to identify
XX whether the antibody has the same binding specificity as the antibodies
XX of the invention. The neutralising antibodies define new epitopes on the
XX HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
XX monoclonal antibodies derives from the fact that they are encoded by a
XX human polynucleotide sequence. Thus in vivo use of the monoclonal
XX antibodies for diagnosis and immunotherapy of HIV induced disease greatly
XX reduces the problems of significant host immune response to the passively
XX administered antibodies which is a problem commonly encountered when
XX monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
XX An additional major advantage of the monoclonal antibodies described
XX derives from the fact that they immunoreact with a unique determinant
XX present on mature HIV glycoprotein gp120. This class of antibodies is
XX particularly effective at neutralising field isolates of HIV
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 3; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
XX 1 ELTQSPSSLSASVGDRTTICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
XX 1 ELTQSPSSLSASVGDRTTICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
XX
XX 61 SGSGYGTDFTLTISSLOQFDEASYCOESLSASVTFQGTGKVEIKR 106
XX 61 SGSGYGTDFTLTISSLOQFDEASYCOESLSASVTFQGTGKLEIKR 106
XX
XX RESULT 6
XX AAG93667
XX ID AAG93667 standard; protein; 107 AA.
XX
XX AAG93667;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH54 protein sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX

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OS Homo sapiens.
XX
XX US62555455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68724.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
XX
XX Claim 1; Col 70; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
XX Sequence 107 AA;
XX
XX Query Match 87.3%; Score 474; DB 4; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 1e-28;
XX Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 ELTQSPSSLSASVGDRTTICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
XX 2 ELTQSPSSMSASVGDRTTICRASQSIGTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
XX
XX 61 SGSGYGTDFTLTISSLOQFDEASYCOESLSASVTFQGTGKVEIKR 106
XX 62 SGSGYGTDFTLTISSLOQFDEASYCOESLSASVTFQGTGKVEIKR 107
XX
XX RESULT 7
XX ABO27474
XX ID ABO27474 standard; protein; 107 AA.
XX
XX ABO27474;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) light chain SH54.
XX
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
XX magnetically activated cell sorting.
XX
XX Homo sapiens.
XX
XX US2003040605-A1.
XX
XX 27-FEB-2003.
XX
XX 04-MAY-2001; 2001US-00848798.
XX

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PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2003-512273/48.
XX N-PSDB; ACD45388.
XX New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
XX Claim 4; Page 53; 187pp; English.
XX The invention relates to an isolated Rh(D) binding protein. The protein
XX can be used for magnetically activated cell sorting. The protein is
XX useful in various diagnostic and therapeutic applications in humans,
XX including typing of blood or blood products. The present sequence
XX represents the amino acid sequence of a human anti-Rh(D) chain
XX Sequence 107 AA;
XX Query Match 87.3%; Score 474; DB 6; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 1e-28;
XX Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ELTQSPSSLSASVGDVRTITCRASQRIYLNWYQHKFGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSMSASVGDVRTITCRASQSIGTYLNWYQKFGKAPKLLIYAASSLQSGVPSRF 61
Qy 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTGKVEIKR 106
Db 62 SGSGGTDFLTITSSLOFEDFATYCOQSYSTPTWTFQGTGKVEIKR 107
RESULT 8
AAG93663
ID AAG93663 standard; protein; 107 AA.
XX AC AAG93663;
XX 14-SEP-2001 (first entry)
XX Human anti-Rh(D) antibody clone SH49 protein sequence.
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68720.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68720.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicines. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX Sequence 107 AA;
XX Query Match 86.9%; Score 472; DB 4; Length 107;
XX Best Local Similarity 86.8%; Pred. No. 1.4e-28;
XX Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSLSASVGDVRTITCRASQRIYLNWYQHKFGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTITCRASQSISSYLNWYQKFGKAPKLLIYAASSLQSGVPSRF 61
Qy 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTGKVEIKR 106
Db 62 SGSGGTDFLTITSSLOFEDFATYCOQSYSTPTWTFQGTGKVEIKR 107
RESULT 9
AAG93664
ID AAG93664 standard; protein; 107 AA.
XX AC AAG93664;
XX 14-SEP-2001 (first entry)
XX Human anti-Rh(D) antibody clone SH50 protein sequence.
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68721.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
XX Claim 1; Col 69; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies

```

CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
 QY 61 SGSGYGTDFTLTISSLQFEDFASYCQESLSASYTFGQGTKEIKR 106
 DB 62 SGSGSGTDFTLTISSLQFEDFATYYCQSQSYSTFWTFGQGTKEIKR 107

RESULT 10
 ID AAG93590 standard; protein; 107 AA.
 XX
 AC AAG93590;

DT 14-SEP-2001 (first entry)
 XX Human anti-Rh(D) chain I02 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.
 XX
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 XX
 XX WPI; 2001-388931/41.
 DR N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Claim 1; Col 43, 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.4e-28;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
 QY 61 SGSGYGTDFTLTISSLQFEDFASYCQESLSASYTFGQGTKEIKR 106
 DB 62 SGSGSGTDFTLTISSLQFEDFATYYCQSQSYSTFWTFGQGTKEIKR 107

RESULT 11
 ID ABO27471 standard; protein; 107 AA.
 XX
 AC ABO27471;

DT 12-SEP-2003 (first entry)
 XX
 DE Anti-Rh(D) light chain SH50.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;
 KW magnetically activated cell sorting.
 XX
 OS Homo sapiens.

XX US2003040605-A1.
 PN
 XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 XX
 XX WPI; 2003-512273/48.
 DR N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 PT
 XX Claim 4; Page 52; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain
 XX
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
 QY 61 SGSGYGTDFTLTISSLQFEDFASYCQESLSASYTFGQGTKEIKR 106
 DB 62 SGSGSGTDFTLTISSLQFEDFATYYCQSQSYSTFWTFGQGTKEIKR 107

```

RESULT 12
ABO27397
ID ABO27397 standard; protein; 107 AA.
XX
XX ABO27397;
AC
XX
XX 12-SEP-2003 (first entry)
DT
XX
XX Anti-Rh(D) chain I02.
DE
XX
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
OS
XX
XX US2003040605-A1.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 04-MAY-2001; 2001US-00848798.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
PR
XX
XX 27-JUN-1997; 97US-00884045.
PR
XX
XX 10-APR-1998; 98US-0081380P.
PR
XX
XX 29-JAN-1999; 99US-00240274.
PR
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2003-512273/48.
DR
XX
XX N-PSDB; ACD45311.
DR
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
PT
XX
XX Claim 4; Page 26; 187pp; English.
PS
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
XX Sequence 107 AA;
SQ
Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLASVGDVRTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDVRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61

Oy 61 SGGSGYGDFTLTITSSLOFEDFASVYCOESLSASVTFQGTKEIKR 106
Db 62 SGGSGYGDFTLTITSSLOFEDFATYCCQSYSTLWTFQGTKEIKR 107

SQ Sequence 107 AA;
Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLASVGDVRTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDVRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61

Oy 61 SGGSGYGDFTLTITSSLOFEDFASVYCOESLSASVTFQGTKEIKR 106
Db 62 SGGSGYGDFTLTITSSLOFEDFATYCCQSYSTLWTFQGTKEIKR 107

RESULT 13
ABO27470
ID ABO27470 standard; protein; 107 AA.
XX
XX ABO27470;
AC
XX
XX 12-SEP-2003 (first entry)
DT
XX
XX Anti-Rh(D) light chain SH49.
DE
XX
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
OS

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XX US2003040505-A1.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 04-MAY-2001; 2001US-00848798.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
PR
XX
XX 27-JUN-1997; 97US-00884045.
PR
XX
XX 10-APR-1998; 98US-0081380P.
PR
XX
XX 29-JAN-1999; 99US-00240274.
PR
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2003-512273/48.
DR
XX
XX N-PSDB; ACD45384.
DR
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
PT
XX
XX Claim 4; Page 52; 187pp; English.
PS
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
XX Sequence 107 AA;
SQ
Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.4e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLASVGDVRTISCRASORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDVRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61

Oy 61 SGGSGYGDFTLTITSSLOFEDFASVYCOESLSASVTFQGTKEIKR 106
Db 62 SGGSGYGDFTLTITSSLOFEDFATYCCQSYSTWTFQGTKEIKR 107

RESULT 14
AAG93644
ID AAG93644 standard; protein; 107 AA.
XX
XX AAG93644;
AC
XX
XX 14-SEP-2001 (first entry)
DT
XX
XX Human anti-Rh(D) antibody clone SH13 protein sequence.
DE
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
OS
XX
XX US6255455-B1.
PN
XX
XX 03-JUL-2001.
PD
XX
XX 29-JAN-1999; 99US-00240274.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
PR
XX
XX 27-JUN-1997; 97US-00884045.
PR
XX
XX 10-APR-1998; 98US-0081380P.
PR
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI

```

XX WPI; 2001-388931/41.
DR N-PSDB; AAH68701.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 68; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93658 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;

Query Match 86.7%; Score 471; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.7e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSRSGVPSRF 61
QY 61 SGGSGYGTDTLTITSSLPQEDFASYCQESLSASVTFGQGTKEIKR 106
DB 62 SGGSGGTDTLTITSSLPQEDFATYCCQSYSTPYTFGQGTKEIKR 107

RESULT 15
ABO27451
ID ABO27451 standard; protein; 107 AA.
XX
AC ABO27451;
DT
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH13.
XX
KW Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
FA
XX Siegel DL;
PI
XX WPI; 2003-512273/48.
DR N-PSDB; ACD45365.
DR
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
PT
XX

PS Claim 4; Page 50; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
XX Sequence 107 AA;
SQ
Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.7e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSRSGVPSRF 61
QY 61 SGGSGYGTDTLTITSSLPQEDFASYCQESLSASVTFGQGTKEIKR 106
DB 62 SGGSGGTDTLTITSSLPQEDFATYCCQSYSTPYTFGQGTKEIKR 107
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 35.8152 Seconds
(without alignments)
928.389 Million cell updates/sec

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	475	87.5	107	14	US-10-016-986-104
3	474	87.3	107	10	US-09-848-798-179
4	472	86.9	107	10	US-09-848-798-33
5	472	86.9	107	10	US-09-848-798-175
6	472	86.9	107	10	US-09-848-798-176
7	471	86.7	107	10	US-09-848-798-156
8	468	86.2	107	10	US-09-848-798-36
9	467	86.0	107	14	US-10-016-986-105
10	465	85.6	111	14	US-10-203-754A-57
11	464.5	85.5	108	10	US-09-848-798-32
12	464.5	85.5	108	10	US-09-848-798-43
13	464	85.5	107	10	US-09-848-798-37
14	464	85.5	240	9	US-09-192-854-2
15	464	85.5	240	9	US-09-968-561A-2

16	454	85.5	240	10	US-09-968-744A-2	Sequence 2, Appli
17	454	85.5	240	12	US-09-968-561A-2	Sequence 2, Appli
18	463	85.3	107	10	US-09-791-153A-67	Sequence 67, Appl
19	462	85.1	106	14	US-10-027-725A-12	Sequence 12, Appl
20	462	85.1	107	10	US-09-848-798-38	Sequence 38, Appl
21	462	85.1	107	10	US-03-848-798-39	Sequence 39, Appl
22	461	84.9	107	10	US-03-848-798-158	Sequence 158, App
23	460.5	84.8	108	10	US-09-848-798-167	Sequence 167, App
24	460	84.7	106	14	US-10-027-725A-11	Sequence 11, Appl
25	459.5	84.6	108	10	US-09-848-798-163	Sequence 163, App
26	458	84.3	107	10	US-09-848-798-35	Sequence 35, Appl
27	458	84.3	107	10	US-02-848-798-173	Sequence 173, App
28	458	84.3	111	14	US-10-203-754A-56	Sequence 56, Appl
29	457	84.2	104	14	US-10-016-986-106	Sequence 106, App
30	457	84.2	107	10	US-09-848-798-40	Sequence 40, Appl
31	457	84.2	214	14	US-10-153-382-19	Sequence 19, Appl
32	456	84.0	107	10	US-09-848-798-44	Sequence 44, Appl
33	455	83.8	107	15	US-10-309-762-88	Sequence 88, Appl
34	454.5	83.7	107	12	US-10-363-349-4	Sequence 7, Appli
35	454.5	83.7	288	12	US-10-663-244-150	Sequence 150, App
36	454	83.6	233	16	US-10-663-244-150	Sequence 172, App
37	452	83.2	107	10	US-09-848-798-172	Sequence 174, App
38	452	83.2	107	10	US-09-848-798-174	Sequence 40, Appl
39	452	83.2	107	15	US-10-723-434-40	Sequence 40, Appl
40	452	83.2	291	12	US-10-406-830-10	Sequence 10, Appl
41	451.5	83.1	108	10	US-09-848-798-41	Sequence 41, Appl
42	451.5	83.1	108	14	US-10-016-986-109	Sequence 109, App
43	451	83.1	107	10	US-09-848-798-168	Sequence 168, App
44	451	83.1	107	15	US-10-309-762-89	Sequence 89, Appl
45	451	83.1	108	12	US-10-371-942-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-027-725A-10
; Sequence 10, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-10

Query Match 100.0%; Score 543; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.7e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVTSICRASORINVLNWKPKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVTSICRASORINVLNWKPKAPKLLIYAASSLSQGVPSRF 60
QY 61 SGSGYGTDFTLTSSIQFEDFASYYCQESLSASYTFGGTKVEIKR 106
Db 61 SGSGYGTDFTLTSSIQFEDFASYYCQESLSASYTFGGTKVEIKR 106

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:

```

; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2C0N1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      87.5%; Score 475; DB 14; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.1e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
QY 61 SSGSGYGTDFTLTISSLOFDFASYCOESLSASVYTFGGTKVEIKR 106
Db 61 SSGSGGTDFTLTISSLOPEDFATYCCQSYSTPTTGGTKLBIKR 106

RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match      87.3%; Score 474; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 5e-37;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

```

```

; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-848-798-33

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.8e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDFTLTISSLOFDFASYCOESLSASVYTFGGTKVEIKR 106
Db 62 SSGSGGTDFTLTISSLOPEDFATYCCQSYSTLWTFGGTKVEIKR 107

RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 7.8e-37;

```

	Matches	92;	Conservative	7;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	ELTQPSLSASVGRVVTISCRASQINTYLNWYQHKPGKAPKLLIYAASSLQSGVSRF	60			:				
Db	2	ELTQPSLSASVGRVVTISCRASQISYLNWYQKQKPGKAPKLLIYAASSLQSGVSRF	61			:				

```

RESULT 6
US-09-848-798-176
; Sequence 176, Application US/09048798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

```

Query Match 86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 7.8e-37;
Matches 92; Conservative 7; Mismatches 7; Indels

Qy	1	ELTQSPSLSASVSGDRVTISCRASQINTYLNWYCHKFGKAPKLLIYAASLSQSGVSRP	60
Db	2	ELTQSPSLSASVSGDRVTIVCRASQISISSYLNWYQKFGKAPKLLIYAASLSQSGVSRP	61
Qy	61	SGSGYGDFLTITISLQDFEDPASYCOESIASYTFGGTKVEIKR	106
Db	62	SGSGYGDFLTITISLQDFEPAIVYCOQSYSTPWFSGTKVEIKR	107

RESULT 7
 US-09-848-798-156
 ; Sequence 156, Application US/09848798
 ; Publication No. US20030040605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; FILE REFERENCE: 09596-42U2
 ; CURRENT APPLICATION NUMBER: US/09/848,798
 ; CURRENT FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 156
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
 US-09-848-798-156

	Query Match	Best Local Similarity	86.7%;	Score 471;	DB 10;	Length 107;
	Matches	92;	Conservative	7;	Mismatches	7;
					Indels	0;
					Gaps	0;
Qy	1	ELTQSPSSLASVGDRTVITSCRAQORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF	60			
Db	2	ELTQSPSSLASVGDRTVITSCRAQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61			
Qy	61	SGSGVGDTFTLTITLSLQPEDFASVYQCSELSASYTFQGTKEIKR	106			
Db	62	SGSGSGDTFTLTITLSLQPEDFATVYQQQSXTPTVFGGTKEIKR	107			

RESULT 8
US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY A
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIORITY FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,0
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,8
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-848-798-16

Query Match	86.2%	Score 468;	DB 10;	Length 107;
Best Local Similarity	86.8%;	Pred. No. 1.8e-36;		
Matches 92;	Conservative 5;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	1	ELTQSPSSLASGVDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIIYAASSLQSGVPSRF	60	
Db	2	ELTQSPSSLASGVDRVTITCRASQSIIRYLNWYQHKPGKAPKLLIIYAASSLQSGVPSRF	61	
Qy	61	SGSGYGTDFLTITSSLOFEPASYCOESIASYTFQGGTKVETKR	106	
Db	62	TGSGSGYGTDFLTITSSLOFEPASYCOOSYSTPQTGGTKVETKR	107	

RESULT 9
US-10-016-986-105
Sequence 105, Application US/10016986
Publication No. US20030187247A1
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016,986
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06

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; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
; OTHER INFORMATION: Sorting Method for Production Thereof
US-09-848-798-32

Query Match      85.5%; Score 464.5; DB 10; Length 108;
Best Local Similarity 86.9%; Pred. No. 4e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGTDFTLTISSLOPEDFASYCQESLSA-SYTFGGQTKVEIKR 106
Db 62 SSGSGTDFTLTISSLOPEDFATYCCQSYSTPTPTFGQTKLEIKR 108

RESULT 12
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; OTHER INFORMATION: Sorting Method for Production Thereof
US-09-848-798-43

Query Match      85.5%; Score 464.5; DB 10; Length 108;
Best Local Similarity 86.9%; Pred. No. 4e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGTDFTLTISSLOPEDFASYCQESLSA-SYTFGGQTKVEIKR 106
Db 62 SSGSGTDFTLTISSLOPEDFATYCCQSYSTPTPTFGQTKLEIKR 108

RESULT 13
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; OTHER INFORMATION: Sorting Method for Production Thereof
US-10-203-754A-57

Query Match      85.6%; Score 465; DB 14; Length 111;
Best Local Similarity 84.8%; Pred. No. 3.7e-36;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 63
QY 62 SSGSGTDFTLTISSLOPEDFASYCQESLSA-SYTFGGQTKVEIKR 106
Db 64 SSGSGTDFTLTISSLOPEDFATYCCQSYSTPTPTFGQTKLEIKR 108

RESULT 11
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; OTHER INFORMATION: Sorting Method for Production Thereof
US-10-203-754A-57
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      85.5%; Score 464; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.4e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVYFGQGTKVEIKR 106
Db 62 SGSGSGTDFTLTISSLOPEDFATYCCQOSYSTPTTFGQGTKLEIKR 107

RESULT 14
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match      85.5%; Score 464; DB 9; Length 240;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 135 QMTQSPSSLSASVGDVRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 194

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVYFGQGTKVEIKR 106
Db 195 SGSGSGTDFTLTISSLOPEDFATYCCQOSYSTPTTFGQGTKVEIKR 240

RESULT 15
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US2002016462A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
```

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; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match      85.5%; Score 464; DB 9; Length 240;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 135 QMTQSPSSLSASVGDVRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 194

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVYFGQGTKVEIKR 106
Db 195 SGSGSGTDFTLTISSLOPEDFATYCCQOSYSTPTTFGQGTKVEIKR 240

Search completed: August 8, 2004, 12:43:21
Job time : 36.8152 secs
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFQGKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	87.5	107	1	US-08-276-852-104
2	475	87.5	107	1	US-08-899-575-104
3	475	87.5	107	1	US-08-899-575-104
4	475	87.5	107	5	PCT-US95-08743-104
5	474	87.3	107	3	US-09-240-274-179
6	472	86.9	107	3	US-09-240-274-33
7	472	86.9	107	3	US-09-240-274-175
8	472	86.9	107	3	US-09-240-274-176
9	471	86.7	107	3	US-09-240-274-156
10	468	86.2	107	3	US-09-240-274-36
11	467	86.0	107	1	US-08-376-852-105
12	467	86.0	107	1	US-08-899-575-105
13	467	86.0	107	1	US-08-899-575-105
14	467	86.0	107	5	PCT-US95-08743-105
15	464.5	85.5	108	3	US-09-240-274-32
16	464.5	85.5	108	3	US-09-240-274-43
17	464	85.5	107	3	US-09-240-274-37
18	462	85.1	107	3	US-09-240-274-38
19	462	85.1	107	3	US-09-240-274-39
20	461	84.9	107	3	US-09-240-274-158
21	460.5	84.8	108	3	US-09-240-274-167
22	459.5	84.6	108	3	US-09-240-274-163
23	458	84.3	107	3	US-09-240-274-35
24	458	84.3	107	3	US-09-240-274-173
25	458	84.3	108	2	US-08-379-057-29
26	457	84.2	104	1	US-08-276-852-106
27	457	84.2	104	1	US-08-899-575-106

28 457 84.2 104 1 US-08-899-575-106 Sequence 106, App
29 457 84.2 104 5 PCT-US95-08743-106 Sequence 106, App
30 457 84.2 107 3 US-09-240-274-40 Sequence 40, Appl
31 457 84.2 214 4 US-09-472-087-71 Sequence 71, Appl
32 456 84.0 107 3 US-09-240-274-44 Sequence 44, Appl
33 452 83.2 107 3 US-09-240-274-172 Sequence 172, App
34 452 83.2 107 3 US-09-240-274-174 Sequence 174, App
35 451.5 83.1 108 1 US-08-276-852-109 Sequence 109, App
36 451.5 83.1 108 1 US-08-899-575-109 Sequence 109, App
37 451.5 83.1 108 1 US-08-899-575-109 Sequence 109, App
38 451.5 83.1 108 3 US-09-240-274-41 Sequence 41, Appl
39 451.5 83.1 108 5 PCT-US95-08743-109 Sequence 109, App
40 451 83.1 107 3 US-09-240-274-168 Sequence 168, App
41 451 83.1 108 4 US-09-025-769B-14 Sequence 14, Appl
42 451 83.1 109 2 US-07-934-373C-3 Sequence 3, Appl
43 451 83.1 109 3 US-08-437-642B-3 Sequence 3, Appl
44 451 83.1 109 4 US-08-146-206C-3 Sequence 3, Appl
45 451 83.1 109 4 US-09-705-686-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRL452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.5e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106
Db 61 SGSGYGTDFLTITSSLOPEDFATYQCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRL452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.5e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106
Db 61 SGSGYGTDFLTITSSLOPEDFATYQCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRL452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.5e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106
Db 61 SGSGYGTDFLTITSSLOPEDFATYQCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743

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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.5e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 1 ELTQSPSSLSASVGDRTVITSCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||

QY 61 SGSGYGTDFLTITSSLOPEDFASYCOESLSASVTFQGGTKVEIKR 106
   |||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCQSYSTPTFTFGGTKVEIKR 106
   |||||

RESULT 5
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.2e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSMSASVGDRTVITCRASQRTIGTLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||

QY 61 SGSGYGTDFLTITSSLOPEDFASYCOESLSASVTFQGGTKVEIKR 106
   |||||
Db 62 SGSGSGTDFLTITSSLOPEDFATYCCQSYSTPTFTFGGTKVEIKR 107
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```

RESULT 6
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.8e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||

QY 61 SGSGYGTDFLTITSSLOPEDFASYCOESLSASVTFQGGTKVEIKR 106
   |||||
Db 62 SGSGSGTDFLTITSSLOPEDFATYCCQSYSTLTWTFGGTKVEIKR 107
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RESULT 7
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||
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QY 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
||||| 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
Db 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107
||||| 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 8
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match 86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
||||| 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61
||||| 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
||||| 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
Db 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107
||||| 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 9
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match 86.7%; Score 471; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
||||| 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61
||||| 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
||||| 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
Db 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107
||||| 62 SSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 10
US-09-240-274-36
; Sequence 36, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-36

Query Match 86.2%; Score 468; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 4.5e-38;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
||||| 1 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61
||||| 2 ELTQSPSSLSASVGDRTVITCRASQIRINTYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
||||| 61 SSGSGYDFTLTISLQDFEASYYCOESLSASYSYTFGQGTKEIKR 106
Db 62 TSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107
||||| 62 TSGSGDFTLTISLQDFEATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 11
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
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; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-105

Query Match      86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQRIINYNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 1 ELTQSPSLASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

QY 61 SGSGYGTDFTLTISSLOFEDFASYCOESLSASVTFGGTKVEIKR 106
Db 61 SGSGYGTDFTLTISSLOFEDFATYYCQSYSTPQTGGTKLEIKR 106

RESULT 12
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-105

Query Match      86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQRIINYNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 1 ELTQSPSLASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

QY 61 SGSGYGTDFTLTISSLOFEDFASYCOESLSASVTFGGTKVEIKR 106
Db 61 SGSGYGTDFTLTISSLOFEDFATYYCQSYSTPQTGGTKLEIKR 106

RESULT 13
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-105

Query Match      86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRASORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
DB 1 ELTQSPSSLASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGSGYGTDFTLTISSLQPEDFASYCQESLSASVYTFQGGTKVEIKR 106
DB 61 SGSGSGTDFTLTISSLQPEDFATYYCQSQSYSTPQTFQGGTKLEIKR 106

RESULT 14
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match      86.0%; Score 467; DB 5; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRASORINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
DB 1 ELTQSPSSLASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGSGYGTDFTLTISSLQPEDFASYCQESLSASVYTFQGGTKVEIKR 106
DB 61 SGSGSGTDFTLTISSLQPEDFATYYCQSQSYSTPQTFQGGTKLEIKR 106

RESULT 15
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 9.31515 Seconds
(without alignments)
1094.593 Million cell updates/sec

Title: US-10-027-725A-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGDRTVTIT.....QQSYTLYTFGSGTKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	85.6	108	2 B49047	Ig kappa chain V r
2	465	85.0	108	2 S47182	Ig kappa chain - h
3	465	85.0	127	2 S40367	Ig kappa chain V-J
4	464	84.8	109	2 S31998	Ig kappa chain - h
5	462	84.5	123	2 S40331	Ig kappa chain - h
6	457	83.5	122	2 S40370	Ig kappa chain - h
7	455	83.2	108	2 S44122	Ig kappa chain V r
8	454	83.0	108	2 S31977	Ig kappa chain - h
9	453	82.8	123	1 KIHUWK	Ig kappa chain pre
10	451	82.4	109	2 S31981	Ig kappa chain - h
11	451	82.4	109	2 S31978	Ig kappa chain - h
12	449	82.1	108	1 KIHUDE	Ig kappa chain V-I
13	447	81.7	108	2 S19674	Ig kappa chain V r
14	446	81.5	129	2 S40317	Ig kappa chain - h
15	438	80.1	117	2 S46371	Ig kappa chain V-J
16	437.5	80.0	106	2 PC2397	anti-tetanus toxin
17	437	79.9	107	2 S36264	Ig lambda chain V
18	437	79.9	108	1 KIHUHU	Ig kappa chain V-I
19	437	79.9	120	2 S46370	Ig kappa chain V-J
20	436	79.7	109	2 S31979	Ig kappa chain - h
21	434	79.3	128	2 S52793	Ig light chain var
22	433	79.2	128	2 S46372	Ig kappa chain V r
23	432	79.0	109	2 S31980	Ig kappa chain - h
24	432	79.0	125	2 S40350	Ig kappa chain - h
25	431	78.8	109	2 S31983	Ig kappa chain - h
26	429	78.4	123	2 S52792	Ig kappa chain V r
27	429	78.4	132	2 S40334	Ig kappa chain - h
28	428	78.2	109	2 S32001	Ig kappa chain - h
29	428	78.2	122	2 S40314	Ig kappa chain - h

ALIGNMENTS

RESULT 1

B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary

A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>

A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 468; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 5.6e-36;
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVTITCRARQISITVLNWOQKPGKAPKLLIWSASNLQSGVPSRF 60

Db 3 QMTQSPSSLSASVGDRTVTITCRASQSISSVLNWOQKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 SGSGSGTEFTLTISNLOQFDFASYCQSYTTLTYTFGSGTKLEIKR 106

Db 63 SGSGSGTDFTLTISLQPEDFATYYCQSYSTPLTFTGGGTKVEIKR 108

RESULT 2

S47182

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47182

R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

Submitted to the EMBL Data Library, June 1994

A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A:Reference number: S47182

A:Accession: S47182

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <NCI>

A:Cross-references: EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID:g506423

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 108;

Oy 62 GSGSGTEFT

SECRET

62 GSGSGTEFTLTISNLQFEDFASYCQSY¹⁰⁶LYTFGSGTKLETKR 106

Accession: S44122

R; Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A; Description: Idiopathic vaccination against human B-cell lymphoma: rescue of variable
A; Reference number: S44105
A; Accession: S44122
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-108 <HAW>
A; Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.L; PID:g940533
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 455; DB 2; Length 108;
Best Local Similarity 84.0%; Pred. No. 8.7e-35;
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRVTITCRARQSISTYLNNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLASVGDRVTITCRASQSISSYLNNWYQQKLGKAPKLLIYSASSLSQGVPSDF 62
QY 61 SGSGSGTEFTLTISNLQFDPASYCCQSYTYLYTFGSGTKLEIKR 106
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
63 SGSGSGTDFTLTISSLQPEDPFIYYCCQSYSTPTWTFGGTKVEIKR 108

RESULT 8
S31977
Ig kappa chain - human
C; Species: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C; Accession: S31977
R; Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
A; Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A; Reference number: S31977
A; Accession: S31977
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-108 <POR>
A; Cross-references: EMBL:Z15073
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 454; DB 2; Length 108;
Best Local Similarity 84.8%; Pred. No. 1.1e-34;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLASVGDRVTITCRARQSISTYLNNWYQQKPGKAPKLLIWSASNLQSGVPSRF 61
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
4 MTQSGSSLASVGDRVTITCRASQSISSYLNNWYQQKPGKAPKLLIYSASSLSQGVPSRF 63
QY 62 GGSGSGTEFTLTISNLQFDPASYCCQSYTYLYTFGSGTKLEIKR 106
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
64 GGSGSGTDFTLTISLQPEDPATYCYCCQSYDTVDTFGGTKVEIKR 108

RESULT 9
XHWUK
Ig kappa chain precursor V-I region (Walker) - human
C; Species: Homo sapiens (man)
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 21-Jan-2000
C; Accession: A01883
R; Klobbeck, H.G.; Combiato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A; Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A; Reference number: A93534; MUID:85014148; PMID:6091049
A; Accession: A01883
A; Molecule type: DNA
A; Residues: 1-129 <KLO>
A; Note: the sequence was determined from the differentiated gene
C; Genetics:

A;Reference number: S31977

A;Accession: S31978

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <PKR>

A;Cross-references: EMBL:Z15074; NID:G38487; PIDN:CAA78783.1; PID:G38488

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;

Best Local Similarity 82.9%; Pred. No. 2e-34;

Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVITTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRFS 61

Db 4 MTQSPSSLSASVGRVITTCRTSQTISRYLNWYQIPGKAPKLLIFAASTLTQTVPSRFG 63

QY 62 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 64 GSGSGTFTLTISTLQPDDEFATYCCQSYTTPYTFGGTKLEIKR 108

RESULT 12

KLHUE

Ig kappa chain V-I region (Dee) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C;Accession: A01865

R;Milstein, C.P.; Deverson, E.V.

Biochem. J. 123, 945-958, 1971

A;Title: The amino acid sequence of a human kappa light chain.

A;Reference number: A01865; MUID:72053133; PMID:5124396

A;Accession: A01865

A;Molecule type: protein

A;Residues: 1-108 <ML>

A;Note: the C region of this chain as the Inv (3) marker

C;Genetics:

A;Gene: GDB:IGKV1

A;Cross-references: GDB:136264

A;Map position: 2p12-2p12

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;16-90/Domain: immunoglobulin homology <IMM>

F;23-88/Disulfide bonds: #status predicted

Query Match 82.1%; Score 449; DB 1; Length 108;

Best Local Similarity 80.2%; Pred. No. 3.1e-34;

Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRFP 60

Db 3 ZMTQSPSSLSASVGRVITTCRAGQSWKYLWYQKPKAPKLLIFAASLLKSGVPSRFP 62

QY 61 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 63 GSGSGTFTLTISGLLPDEFATYCCQSYTTPYTFGGTKVEMTR 108

RESULT 13

SI9674

Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C;Accession: S19674

R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,

J. Mol. Biol. 222, 591-597, 1991

A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A;Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19674

A;Molecule type: mRNA

A;Residues: 1-108 <VAR>

A;Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:gl333586

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 447; DB 2; Length 108;

Best Local Similarity 83.8%; Pred. No. 4.7e-34;

Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVITTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRFS 61

Db 4 LTQSPSSLSASVGRVITTCRARSISITLWYQKPKAPKLLIYAASTLQSGVPSRFS 63

QY 62 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 64 GSGSGTFTLTINSLOQDEFATYCCQNTSPLTFGGGTKEIKR 108

RESULT 14

S40317

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40317

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40317

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLE>

A;Cross-references: EMBL:X72427; NID:G441322; PIDN:CAA51095.1; PID:G441323

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;37-111/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.5%; Score 446; DB 2; Length 129;

Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRFP 60

Db 24 QMTQSPSSLSLSTSLGDRVITTCRASQSIGTLYWYQKPKAPKFLIYGASSLQSGVPSRFP 83

QY 61 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIK 105

Db 84 GSGSGTFTLTISLQPEDFATYCCQTYSTPTTFGGTKVEIK 128

RESULT 15

S46371

Ig kappa chain V-J region (T24-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C;Accession: S46371; S38645

R;Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re

A;Reference number: S46369; MUID:94313975; PMID:8039491

A;Accession: S46371

A;Molecule type: mRNA

A;Residues: 1-117 <BEN>

A;Cross-references: EMBL:Z27172; NID:G415959; PIDN:CAA81696.1; PID:G415960

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;23-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 80.1%; Score 438; DB 2; Length 117;

Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: August 8, 2004, 12:09:01 ; Search time 5.78182 Seconds
(without alignments)
954.620 Million cell updates/sec
Title: US-10-027-725a-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGRVTIT.....QQSYTTLTYFGSGTKLEIKR 106
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	82.8	129	1 KV1W HUMAN	P04431 homo sapien
2	449	82.1	108	1 KV1E HUMAN	P01597 homo sapien
3	437	79.9	108	1 KV1H HUMAN	P01600 homo sapien
4	424	77.5	108	1 KV1N HUMAN	P01606 homo sapien
5	416	76.1	108	1 KV1B HUMAN	P01594 homo sapien
6	416	76.1	108	1 KV1O HUMAN	P01607 homo sapien
7	413.5	75.6	107	1 KV1D HUMAN	P01596 homo sapien
8	412	75.3	129	1 KV1X HUMAN	P04432 homo sapien
9	411.5	75.2	109	1 KV1T HUMAN	P01612 homo sapien
10	411	75.1	108	1 KV1S HUMAN	P01611 homo sapien
11	408	74.6	108	1 KV1V HUMAN	P04430 homo sapien
12	407	74.4	108	1 KV1P HUMAN	P01598 homo sapien
13	403	73.7	108	1 KV1F HUMAN	P01608 homo sapien
14	402	73.5	108	1 KV1A HUMAN	P01593 homo sapien
15	402	73.5	108	1 KV1G HUMAN	P01599 homo sapien
16	401	73.3	108	1 KV1L HUMAN	P01604 homo sapien
17	401	73.3	108	1 KV1Y HUMAN	P80362 homo sapien
18	399	72.9	108	1 KV1R HUMAN	P01610 homo sapien
19	396	72.4	108	1 KV1C HUMAN	P01595 homo sapien
20	395	72.2	108	1 KV1M HUMAN	P01605 homo sapien
21	393	71.8	108	1 KV1K HUMAN	P01603 homo sapien
22	384	70.2	108	1 KV1Q HUMAN	P01609 homo sapien
23	384	70.2	108	1 KV5M MOUSE	P01646 mus musculus
24	383	70.0	117	1 KV1J HUMAN	P01602 homo sapien
25	377	68.9	117	1 KV1I HUMAN	P01601 homo sapien
26	375	68.6	108	1 KV5N MOUSE	P01647 mus musculus
27	374	68.4	108	1 KV5K MOUSE	P01644 mus musculus
28	373	68.2	108	1 KV5D MOUSE	P01645 mus musculus
29	372	68.0	108	1 KV5L MOUSE	P01652 mus musculus
30	372	68.0	108	1 KV5S MOUSE	P01625 homo sapien
31	372	68.0	114	1 KV4A HUMAN	P01648 mus musculus
32	371	67.8	108	1 KV5O MOUSE	P01665 mus musculus
33	371	67.8	111	1 KV3M MOUSE	

34	370	67.6	111	1 KV3O MOUSE	P01657 mus musculus
35	368	67.3	111	1 KV3L MOUSE	P01664 mus musculus
36	367	67.1	108	1 KV5P MOUSE	P01649 mus musculus
37	366	66.9	111	1 KV3Q MOUSE	P01669 mus musculus
38	366	66.9	149	1 KV5A MOUSE	P01633 mus musculus
39	365	66.7	136	1 KV5E MOUSE	P01634 mus musculus
40	364.5	66.6	129	1 KV3J HUMAN	P18135 homo sapien
41	363	66.4	108	1 KV3U MOUSE	P01650 mus musculus
42	362	66.2	111	1 KV3H MOUSE	P01660 mus musculus
43	362	66.2	111	1 KV3N MOUSE	P01666 mus musculus
44	362	66.2	134	1 KV4C HUMAN	P06314 homo sapien
45	361	66.0	108	1 KV5U MOUSE	P04946 mus musculus

ALIGNMENTS

RESULT 1

KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
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EMBL; X00965; CAA25477.1; ALT_TERM.
PIR; A01883; KIHUWK.
HSP; P01607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig_v.
SMART; SM00406; Ig_v.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 22
CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
DOMAIN 23 45 FRAMEWORK-1.
DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 57 71 FRAMEWORK-2.
DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 79 110 FRAMEWORK-3.
DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
DOMAIN 120 129 FRAMEWORK-4.
DISULFID 45 110 BY SIMILARITY.
NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;
Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 1.2e-40;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUHU.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 4,7e-39;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLPSGVPSRF 62
QY 61 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIKR 108

RESULT 4
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains.";
RL Science 169:56-59 (1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
CC PIR; A01872; KIHUOU.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.

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QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVTSRF 84
QY 61 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIK 105
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIK 129

RESULT 2
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958 (1971).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01865; KIHUDE.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.6e-40;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 ZMTQSPSSLSASVGDRTVITTCRASQSVNKNYLNWYQKPGKAPKLLIYAASLQSGVPSRF 62
QY 61 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 SSGSGTFTLTISNLFQEDFASYCQSYTLYTFGSGTKLEIKR 108

RESULT 3
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).

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DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON TER 108 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;
 Query Match 77.5%; Score 424; DB 1; Length 108;
 Best Local Similarity 68.9%; Pred. No. 1.1e-37;
 Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSLASVGDVRVITICRAQSIYSTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
 Db :::::::::::::::::::::::::::::
 3 QMTSPSLASVGDVRVITICRASTZTSSLEWZZKPKAPBLIIYAASBLHSGVPSRF 62
 QY 61 SGSGSGTEFTLTISNLOFEDFASYCQSYTYLTFTGSGTKLEIKR 106
 Db :::::::::::::::::::::::::::::
 63 SGSGSGTEFTLTISLZPBFATYCYZSYSSPTFTFGZGTRLZIKR 108
 RESULT 5
 KV10 HUMAN
 ID KV10 HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiehl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 DR PIR; A91653; KIHUAV.
 DR PDB; 1JW5; 30-JAN-02.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON TER 108 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6B9 CRC64;
 Query Match 76.1%; Score 416; DB 1; Length 108;
 Best Local Similarity 76.4%; Pred. No. 7.5e-37;
 Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ELTQSPSLASVGDVRVITICRAQSIYSTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
 Db :::::::::::::::::::::::::::::::
 3 QMTQSPSLASVGDVRVITICRAQSDISDYLNWYQKPKAPKLLIYDASNLQSGVPSRF 62
 QY 61 SGSGSGTEFTLTISNLOFEDFASYCQSYTYLTFTGSGTKLEIKR 106
 Db :::::::::::::::::::::::::::::::
 63 SGSGSGTEFTLTISLQPDIAITYCQYDYLPTFTGGQTKVEIKR 108
 RESULT 6
 KV10 HUMAN
 ID KV10 HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rei.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the
 three-dimensional structure of antibodies, in particular their
 combining site.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein Rei refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91663; KIHURE.
 DR PDB; 1REI; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BW2; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Glycoprotein. N-LINKED (GLCNAC. . .).
FT CARBOHYD 28 28
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 75.6%; Score 413.5; DB 1; Length 107;
Best Local Similarity 72.6%; Pred. No. 1.4e-36;
Matches 77; Conservative 20; Mismatches 8; Indels 1; Gaps 1;

QY 1 ELTQPSSLSASGVRVTITTCRAGSISFLNMYQQKPGKAPKLLIWSASNLOSQGVPSRF 60
DB 3 QNTQSPSTLSASGVRVAITCRASQNSISSLAWYQQKPGKAPKVLIYKSSLSQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLQFEDFASYQCQSYYTLTYTFGSQTKLEIKR 106
DB 63 SGSGSGTDFTLTISSLZPBBFATYYCQ-YNTFFTEGPGTKVDIKR 107

RESULT 8
KVIX HUMAN STANDARD; PRT; 129 AA.
ID_KVIX_HUMAN
AC P04372;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE ig kappa chain V-I region Daudi precursor.
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combiato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related."
RT Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; KIHUDI.
DR HSPSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22 IG KAPPA CHAIN V-I REGION DAUDI.
FT CHAIN 23 129 FRAMEWORK-1.
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 111 119 FRAMEWORK-4.
FT DOMAIN 120 129 BY SIMILARITY.
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAP076BCTB5574C8 CRC64;

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Query Match      75.3%; Score 412; DB 1; Length 129;
Best Local Similarity 74.3%; Pred. No. 2.4e-36;
Matches 78; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 QMTQSPSSLSASVGRVITTCRAGNITNFLSWYQKPGKAPKLLIYAVSNLQGVPSRF 84
OS :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGSGTEFTLTISNLFQEDFASYYCQSYTYTLTYFGSGTKLEIK 105
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 SGSGSGTEFTLTISNLFQEDFATFYCQSYTNFSTFGGGTKVDNK 129

RESULT 9
KVIT_HUMAN
ID KVIT_HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region Mv.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic
Bence-Jones Protein (Mv). An unusual insertion in the third
RT hypervariable region of a human kappa-immunoglobulin light chain."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC FOUND.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01879; KIHUMV.
DR HSP; P80362; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11870 MW; B6ABF451D55F5A0 CRC64;

Query Match      75.2%; Score 411.5; DB 1; Length 109;
Best Local Similarity 76.8%; Pred. No. 2.3e-36;
Matches 82; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QMTQSPSSLSASVGRVITTCRASQSDYLNWYQKPGKAPKLLIFDTSNLQSGVPSRF 62
QY 61 SGSGSGTEFTLTISNLFQEDFASYYCQSYTYT-LYTFGSGTKLEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 SGSGSGTEFTLTISNLFQEDFATFYCQSYTNPEVTFGGGTTVDIKR 109

RESULT 10
KVIT_HUMAN
ID KVIT_HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region Mv.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";

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RL Mol. Immunol. 23:73-78 (1986).
DR PIR; A01878; KIHUEN.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 74.6%; Score 408; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 5.2e-36;
Matches 79; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 QLTQSPSLASVGDRTVITCRASQSYVYVAWFQKPGKAPKSLIYDASTLQSGVPSNF 62

QY 61 SGSGSGTEFTLTISNLPEDFASYCQSYTYLTNFGSGTKLEIKR 106
DB 63 TGSGSGTDFILTISSLPEDFATYCCQYNSYPTFGQGTQVQIKR 108

RESULT 12
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottleib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]_
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHUEN.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 74.4%; Score 407; DB 1; Length 108;
Best Local Similarity 74.3%; Pred. No. 6.6e-36;
Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQSINTLWLAQQKPGKAPKLLMYKASSLESQVPSRF 62

QY 61 SGSGSGTEFTLTISNLPEDFASYCQSYTYLTNFGSGTKLEIK 105
DB 63 IGSGSGTEFTLTISLPEDFATYCCQYNSDSKMFQGTQVVK 107

RESULT 13
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RA "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]_
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.

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FT  DISULFID 23 88 BY SIMILARITY.
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11782 MW; 53ACEDE5A313DF3A CRC64;

Query Match 73.7%; Score 403; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 1.7e-35;
Matches 77; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIWDASNLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLQFDEASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGTSGTDFTFITISLQPEDATYTCQDFNLTFFGGTKVDFKR 108

RESULT 14
KV1A_HUMAN
ID  KV1A_HUMAN STANDARD; PRT; 108 AA.
AC  P01593;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-I region AG.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=69234734; PubMed=4893682;
RA  Titani K., Shinoda T., Putnam F.W.;
RT  "The amino acid sequence and location of a kappa type Bence-Jones protein. 3. The
RT  complete sequence and the location of the disulfide bridges.";
RL  J. Biol. Chem. 244:3550-3560(1969).
CC  -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR  PIR; A01861; KIHUAG.
DR  HSSP; P01607; IREI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region; Bence-Jones protein.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 35 49 FRAMEWORK-2.
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 57 88 FRAMEWORK-3.
FT  DOMAIN 89 97 FRAMEWORK-4.
FT  DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT  DISULFID 23 88 FRAMEWORK-4.
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 2.2e-35;
Matches 79; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIYDASNLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLQFDEASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGSGGTDFTFITISLQPEDATYTCQYDTLPTFFGGTKLEIKR 108
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RESULT 15
KV1G_HUMAN
ID  KV1G_HUMAN STANDARD; PRT; 108 AA.
AC  P01599;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-I region Gal.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=75059122; PubMed=4215718;
RA  Laure C.J., Watanabe S., Hilschmann N.;
RT  "The primary structure of a monoclonal IgM-immunoglobulin
RT  (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT  kappa-type, subgroup I.";
RL  Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC  -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC  MACROGLOBULIN.
DR  PIR; A01867; KIHUGL.
DR  HSSP; P01607; IREI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 35 49 FRAMEWORK-2.
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 57 88 FRAMEWORK-3.
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON_TER 108
SQ  SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;
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Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 2.2e-35;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCARQISITLWYQKPGKAPKLLIYDASNLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLQFDEASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGSGAGTEFTLTISLQPEDATYTCQQNSYPSRFGQGTKEIKR 108
```

Search completed: August 8, 2004, 12:14:32
Job time : 5.78182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 29.0697 Seconds
(without alignments)
1150.508 Million cell updates/sec

Title: US-10-027-725A-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGDRTVT.....QQSYTILYFGSGKGLRIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	467	85.4	108	4 Q9UL77	Q9ul77 homo sapien
2	465.5	85.1	107	4 Q96SA9	Q96sa9 homo sapien
3	448.5	82.0	107	4 Q9UL81	Q9ul81 homo sapien
4	423	77.3	234	4 Q7Z473	Q7z473 homo sapien
5	414	75.7	108	4 Q9UL70	Q9ul70 homo sapien
6	413	75.5	108	4 Q9UL79	Q9ul79 homo sapien
7	408	74.6	236	4 Q7Z3Y4	Q7z3y4 homo sapien
8	387	70.7	298	11 Q9QYF0	Q9qyf0 mus musculus
9	379	69.3	234	11 Q9LWF8	Q9lwf8 mus musculus
10	374	68.4	116	4 Q96PF6	Q96pf6 homo sapien
11	374	68.4	234	11 Q9R062	Q9r062 mus musculus
12	373	68.2	109	11 Q920E6	Q920e6 mus musculus
13	371	67.8	108	4 Q9UL83	Q9ul83 homo sapien
14	368	67.3	214	11 Q9RIAS	Q9ria5 mus musculus
15	367	67.1	234	11 Q8VCP0	Q8vcp0 mus musculus
16	366	66.9	111	11 Q920E9	Q920e9 mus musculus

ALIGNMENTS

RESULT 1

Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; --
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 85.4%; Score 467; DB 4; Length 108;
Best Local Similarity 84.0%; Pred. No. 2e-44;
Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTTCRARQSIISTYLNWYQQKFGKAPKLLIWSASNLQSGVPSRF 60

Q7tmk3 mus musculus
Q9lws9 mus musculus
Q8vi30 mus musculus
Q8liu6 mus musculus
Q7ts98 mus musculus
Q8klf1 mus musculus
Q9ul85 homo sapien
Q9ul78 homo sapien
Q8klf2 mus musculus
Q7tm2 mus musculus
Q9ul86 homo sapien
Q8klf3 mus musculus
Q8li1c3 mus musculus
Q9er29 mus musculus
Q9gm37 mus musculus
Q9u410 schistosoma
Q8vdd0 mus musculus
Q9jl74 mus musculus
Q7tmk0 mus musculus
Q92ia6 mus musculus
Q9jl84 mus musculus
Q8vci6 mus musculus
Q9jl76 mus musculus
Q9jl78 mus musculus
Q92ts9 mus musculus
Q8vcs5 mus musculus
Q9jl80 mus musculus
Q7sz36 xenopus lae
Q8klf0 mus musculus

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR ENBL; AF035033; AAD56269.1; -.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 107 107
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 4; Length 107;
 Best Local Similarity 82.1%; Pred. No. 2.3e-42;
 Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Oy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGSGSGTDFLTISGLQEDFATYVCOQSYTTLTYFGSGTKLEIKR 107

RESULT 4
 Q2473 PRELIMINARY; PRT; 234 AA.

ID Q2473
 AC Q2473;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC056256; AAB56256.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.3%; Score 423; DB 4; Length 234;
 Best Local Similarity 77.3%; Pred. No. 2.3e-42;
 Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Oy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGSGSGTDFLTISGLQEDFATYVCOQSYTTLTYFGSGTKLEIKR 107

RESULT 4
 Q2473 PRELIMINARY; PRT; 234 AA.

ID Q2473
 AC Q2473;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC056256; AAB56256.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.3%; Score 423; DB 4; Length 234;
 Best Local Similarity 77.3%; Pred. No. 2.3e-42;
 Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Oy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGSGSGTDFLTISGLQEDFATYVCOQSYTTLTYFGSGTKLEIKR 107

RESULT 3
 Q9UL81 PRELIMINARY; PRT; 107 AA.

ID Q9UL81
 AC Q9UL81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;

Query Match 85.1%; Score 465.5; DB 4; Length 107;
 Best Local Similarity 85.8%; Pred. No. 3e-44; 3; Indels 1; Gaps 1;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

Oy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGSGSGTDFLTISGLQEDFATYVCOQSYTTLTYFGSGTKLEIKR 107

RESULT 3
 Q9UL81 PRELIMINARY; PRT; 107 AA.

ID Q9UL81
 AC Q9UL81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;

Query Match 85.1%; Score 465.5; DB 4; Length 107;
 Best Local Similarity 85.8%; Pred. No. 3e-44; 3; Indels 1; Gaps 1;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

Oy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGSGSGTDFLTISGLQEDFATYVCOQSYTTLTYFGSGTKLEIKR 107


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Best Local Similarity 78.1%; Pred. No. 4.5e-39;
Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRARQISITLYNWYQKPGKAPKLLIWSASNLQSGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 MTQSPSSFSASVGDRTVITCRASQISGLYAWYQKPGKAPQLIYAASLTQSGVPSRFS 83
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GSGSGTEFTLTISNLQFEDFASYCQSQSYTYTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 GSASGTDFTLTISLCLOSEDFATYCCQYTYTPWTFGGTKVEIKR 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 75.5%; Score 413; DB 4; Length 108;
Best Local Similarity 77.1%; Pred. No. 2.2e-38;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRARQISITLYNWYQKPGKAPKLLIWSASNLQSGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 MTQSPSSLSASVGDRTVITCRMSQGISYLAWYQKPGKAPQLIYAASLTQSGVPSRFS 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GSGSGTEFTLTISNLQFEDFASYCQSQSYTYTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 GSGSGTDFTLTISLCLOSEDFATYCCQYTYTPWTFGGTKVEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshysuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC005332; AAH05332.1; -.

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Best Local Similarity 78.1%; Pred. No. 4.5e-39;
Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRARQISITLYNWYQKPGKAPKLLIWSASNLQSGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 MTQSPSSFSASVGDRTVITCRASQISGLYAWYQKPGKAPQLIYAASLTQSGVPSRFS 83
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GSGSGTEFTLTISNLQFEDFASYCQSQSYTYTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 GSASGTDFTLTISLCLOSEDFATYCCQYTYTPWTFGGTKVEIKR 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 75.7%; Score 414; DB 4; Length 108;
Best Local Similarity 77.4%; Pred. No. 1.7e-38;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLSASVGDRTVITCRASQISGLYAWYQKPGKAPQLIYAASLTQSGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GSGSGTEFTLTISNLQFEDFASYCQSQSYTYTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 GSGSGTDFTLTISLCLOSEDFATYCCQYTYTPWTFGGTKVEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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Db 3 QMTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 62
 QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYTSGGTKLEIKR 106
 Db 63 SGGSGATNFVTISSLQFEDFATYCCQYHLLPFTFGTKVDPKR 108

RESULT 11

Q8R062 ID Q8R062 PRELIMINARY; PRT; 234 AA.
 AC Q8R062
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Colon;
 RA Strauberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027418; AAH27418.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_
 SQ SEQUENCE 234 AA; 25857 MW; 4E08C81426AEAB1 CRC64;

Query Match 68.4%; Score 374; DB 11; Length 234;
 Best Local Similarity 69.8%; Pred. No. 1.3e-33;
 Matches 74; Conservative 12; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 23 QMTQSSLSASVGDRTVITCRARQISITVLYNWYQKPGDGTGKLLIYTTSSLHSGVPSRF 82
 QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYTSGGTKLEIKR 106
 Db 83 SGGSGGTHSLTISNLEPEDIAIYCCQYSGFFFTFGGTKLEIKR 128

RESULT 12

Q920E6 ID Q920E6 PRELIMINARY; PRT; 109 AA.
 AC Q920E6
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotope kappa chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
 in Mammalian Cells."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307938; AAL09422.1; -.
 DR PIR; S19112; S19112.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
 Query Match 68.2%; Score 373; DB 11; Length 109;
 Best Local Similarity 66.0%; Pred. No. 6.6e-34;
 Matches 70; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 3 QMTQSPASLSASVGEVTITCRASGNIHNLVYQKQKSPQLLYVYNAKTLADGVPSRF 62
 QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYTSGGTKLEIKR 106
 Db 63 SGGSGGTQVSLKINSLQPEDFGSYCQHFWSWTFGGTKLEIKR 108

RESULT 13

Q9UL83 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
 AC Q9UL83
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035031; AAD56267.1; -.
 DR PIR; B30609; B30609.
 DR PIR; C30609; C30609.
 DR PIR; D30609; D30609.
 DR PIR; S34098; S34098.
 DR PIR; S34099; S34099.
 DR HSSP; P80362; LWTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 67.8%; Score 371; DB 4; Length 108;
 Best Local Similarity 65.7%; Pred. No. 1.1e-33;
 Matches 69; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
 QY 2 LTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
 Db 4 MTQSFATLSVSGERATLSCRASQSVSSNLAWYQKPGQAPRELLYCASTRATGIPARF 63
 QY 62 GSGSGTEFTLTISNLQFEDFASYCQSYTTLTYTSGGTKLEIKR 106
 Db 64 GSGSGTEFTLTISNLQFEDFAVYCYCHYNNWPFTEGPGTKVDIKR 108

RESULT 14

Q9RIA5 ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
 AC Q9RIA5
 DT 01-MAY-2000 (Tremblrel. 13, Created)

```
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR PDB; 1C1C; 11-MAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K6Q; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
```

```
Query Match 67.3%; Score 368; DB 11; Length 214;
Best Local Similarity 65.1%; Pred. No. 5.6e-33;
Matches 69; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 QLTQSPASLSASVGEIVTITCRASENIYSYLVANYQQQKSPQLLYNNAKTLDAGVPSRF 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGGTFTLTISNLQFEDFASYCQOSYTTLTITFGSGTKLEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 SGRSGGTQFSLKINSIQPEDFGSYCQHHSGIPFTFGSGTKLEIKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Search completed: August 8, 2004, 12:17:46
Job time : 29.0697 secs

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RESULT 15
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 67.1%; Score 367; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 8.1e-33;
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 43.5242 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGDRVTIT.....QQSVTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	537	98.2	106	5	ABG30449	Abg30449 Human Ige
2	484	88.5	107	2	AAR54260	Aar54260 Anti-Hiv
3	484	88.5	107	2	AAW01283	Aaw01283 VL region
4	484	88.5	107	3	AAV98244	Aay98244 Anti-gp12
5	484	88.5	107	3	AAV95135	Aay95135 Anti-gp12
6	483	88.3	107	4	AAG93590	Aag93590 Human ant
7	483	88.3	107	6	ABO27397	AbO27397 Anti-Rh(D
8	480	87.8	107	4	AAG93644	Aag93644 Human ant
9	480	87.8	107	6	ABO27451	AbO27451 Anti-Rh(D
10	476	87.0	107	2	AAR54261	Aar54261 Anti-Hiv
11	476	87.0	107	2	AAW01284	Aaw01284 VL region
12	476	87.0	107	3	AAV98245	Aay98245 Anti-gp12
13	476	87.0	107	3	AAV95136	Aay95136 Anti-gp12
14	475	86.8	107	4	AAG93663	Aag93663 Human ant
15	475	86.8	107	4	AAG93664	Aag93664 Human ant
16	475	86.8	107	6	ABO27471	AbO27471 Anti-Rh(D
17	475	86.8	107	6	ABO27470	AbO27470 Anti-Rh(D
18	474	86.7	107	4	AAG93667	Aag93667 Human ant
19	474	86.7	107	6	ABO27474	AbO27474 Anti-Rh(D
20	473.5	86.6	108	4	AAG93589	Aag93589 Human ant
21	473.5	86.6	108	4	AAG93600	Aag93600 Human ant
22	473.5	86.6	108	6	ABO27407	AbO27407 Anti-Rh(D
23	473.5	86.6	108	6	ABO27396	AbO27396 Anti-Rh(D
24	473	86.5	107	4	AAG93594	Aag93594 Human ant
25	473	86.5	107	6	ABO27401	AbO27401 Anti-Rh(D

26	473	86.5	111	4	AAG63656	Aag63656 Amino aci
27	473	86.5	111	6	ABJ38615	Abj38615 Hepatitis
28	473	86.5	240	6	ABJ38595	Abj38595 Hepatitis
29	473	86.5	299	4	AAG63660	Aag63660 Amino aci
30	472.5	86.4	108	4	AAG93655	Aag93655 Human ant
31	472.5	86.4	108	6	ABO27462	AbO27462 Anti-Rh(D
32	472	86.3	107	4	AAG93596	Aag93596 Human ant
33	472	86.3	107	4	AAG93650	Aag93650 Human ant
34	472	86.3	107	4	AAG93595	Aag93595 Human ant
35	472	86.3	107	6	ABO27457	AbO27457 Anti-Rh(D
36	472	86.3	107	6	ABO27403	AbO27403 Anti-Rh(D
37	472	86.3	107	6	ABO27402	AbO27402 Anti-Rh(D
38	471	86.1	107	4	AAG93646	Aag93646 Human ant
39	471	86.1	107	6	ABO27453	AbO27453 Anti-Rh(D
40	470	85.9	108	6	AAO16704	Aao16704 Human ant
41	470	85.9	108	6	AAO16706	Aao16706 Human ant
42	470	85.9	114	2	AAW13922	Aaw13922 Light cha
43	469	85.7	107	4	AAG93601	Aag93601 Human ant
44	469	85.7	107	6	ABO27408	AbO27408 Anti-Rh(D
45	468	85.6	111	4	AAG63655	Aag63655 Amino aci

ALIGNMENTS

RESULT 1
ABG30449
ID AEG30449 standard; protein; 106 AA.
XX AC ABG30449;
XX AC
DT 21-OCT-2002 (first entry)
XX
DE Human Ige Fab clone 60 light chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Region	1..21
FT	Region	/note= "FR1 region"
FT	Region	22..32
FT	Region	/note= "CDR1 region"
FT	Region	33..47
FT	Region	/note= "FR2 region"
FT	Region	48..54
FT	Region	/note= "CDR2 protein"
FT	Region	55..86
FT	Region	/note= "FR3 region"
FT	Region	87..95
FT	Region	/note= "CDR2 region"
FT	Region	96..104
FT	Misc-difference	/note= "FR4 region"
FT	Misc-difference	98
FT	Misc-difference	/note= "Encoded by CCT"
XX	WO200253595-A1.	

11-JUL-2002.
27-DEC-2001; 2001WO-SE002908.
29-DEC-2000; 2000SE-00004892.
(PHNA) PHARMACIA DIAGNOSTICS AB.
PI Flicker S, Steinberger P, Kraft D, Valenta R;
DR WPI; 2002-583604/62.
DR N-PSDB; ABK89641.
XX

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 FT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.
 XX
 XX
 PS Disclosure; Page 40; 45pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergen's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
 CC fab, clone 60 light chain protein of the invention
 XX
 SQ Sequence 106 AA;

Query Match 98.2%; Score 537; DB 5; Length 106;
 Best Local Similarity 99.1%; Pred. No. 4.4e-30;
 Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSLASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
 DB 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 2
 AAR54260
 ID AAR54260 standard; protein; 107 AA.
 XX
 AC AAR54260;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1994 (first entry)
 XX
 DT Anti-HIV gp120 immunoglobulin light chain variable region b22.
 DE
 XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain; variable region;
 KW framework; complementarity determining region.
 XX
 OS Homo sapiens.

Key	Location/Qualifiers
Region	1..21 /label= FR1
Region	22..33 /label= CDR1
Region	34..48 /label= FR2
Region	49..55 /label= CDR2
Region	56..87 /label= FR3
Region	88..95 /label= CDR3
Region	96..107 /label= FR4

WO9407922-A1.

PD 14-APR-1994.
 XX
 PF 30-SEP-1993; 93WO-US0009328.
 XX
 PF 30-SEP-1992; 92US-00954148.
 XX
 PA (SCRI) SRIIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 1994-135516/16.
 XX
 PT New human monoclonal antibodies neutralising HIV - react with gp120 or
 PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
 PT diagnosis and for passive immuno-therapy.
 XX
 PS Claim 5; Page 189; 248pp; English.
 XX
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
 CC using primers specific for heavy and light chain variable regions. The
 CC amplification products were inserted into a dicistronic vector to produce
 CC a library of fragments. E.coli XL1 Blue cells were transformed with the
 CC library. Filamentous phage were produced which expressed the MAB regions
 CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
 CC immunoreactive clones. The light chain VK region sequence AAR54260
 CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 107 AA;

Query Match 88.5%; Score 484; DB 2; Length 107;
 Best Local Similarity 88.7%; Pred. No. 2e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSLASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
 DB 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 3
 AAW01283
 ID AAW01283 standard; protein; 107 AA.
 XX
 AC AAW01283;
 XX
 DT 29-JAN-1997 (first entry)
 XX
 DE VL region of HIV neutralising MAB, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.

Key	Location/Qualifiers
Region	1..21 /label= FR1
Region	22..32 /label= CDR1
Region	33..47 /label= FR2
Region	48..54 /label= CDR2
Region	55..86 /label= FR3
Region	87..95 /label= CDR3
Region	96..107

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FT XX /label= FR4
PN XX WO9602273-A1.
PD XX 01-FEB-1996.
XX PF 11-JUL-1995; 95WO-US008743.
XX PR 18-JUL-1994; 94US-00276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1996-179601/18.
XX PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
XX PS Example; Fig 11; 366pp; English.
XX CC The sequences given in AA01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2 gene
CC clones, b22 and B35. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
CC mature gp120 preferentially over the precursor gp160. The Mab may be used
CC for determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX SQ Sequence 107 AA;

Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSTLYLNWYQKPGKAPKLLIYASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGSGSGTFTLTISNLQFEDFASYCQSYTYTLTYFGSGTKLEIKR 106
DB 61 SGSGSGTFTLTISLQPEDFATYYCQSYSTPYTFGGTKLEIKR 106

RESULT 4
AA98244
ID AAY98244 standard; protein; 107 AA.
XX AC AAY98244;
XX DT 04-JUL-2000 (first entry)
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX OS Homo sapiens.
XX PN AU9948754-A.
XX PD 17-FEB-2000.
XX PF 16-SEP-1999; 99AU-00048754.
XX PR 16-SEP-1999; 99AU-00048754.
XX PA (SCRI ) SCRIPPS RES INST.

```

```

XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 2000-246867/22.
XX PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX Glycoprotein-120.
XX PS Example 9; Fig 11; 374pp; English.
XX CC This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AA98206) and a
XX second polynucleotide encoding a light chain immunoglobulin amino acid
XX sequence; (b) inserting the first and second polynucleotide sequences
XX into a host cell; (c) maintaining the host cell in conditions which allow
XX the amino acid sequences encoded by the polynucleotides to be expressed
XX in the host cell; and (d) isolating the antibody comprising the heavy and
XX light chain immunoglobulin amino acid sequences from the host cell. The
XX anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used for
XX neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting HIV
XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the antibodies
XX associated with monoclonal antibodies of xenogeneic or chimeric
XX derivation
XX SQ Sequence 107 AA;

Query Match 88.5%; Score 484; DB 3; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSTLYLNWYQKPGKAPKLLIYASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGSGSGTFTLTISNLQFEDFASYCQSYTYTLTYFGSGTKLEIKR 106
DB 61 SGSGSGTFTLTISLQPEDFATYYCQSYSTPYTFGGTKLEIKR 106

RESULT 5
AA95135
ID AAY95135 standard; protein; 107 AA.
XX AC AAY95135;
XX DT 30-JUN-2000 (first entry)
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX OS Homo sapiens.

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XX AU9948756-A.
 PN 17-FEB-2000.
 PD 16-SEP-1999; 99AU-00048756.
 PF 16-SEP-1999; 99AU-00048756.
 PR (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 XX WFI; 2000-293393/26.
 XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX Example 9; Fig 11; 366pp; English.
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX Sequence 107 AA;
 SQ Query Match 88.5%; Score 484; DB 3; Length 107;
 Best Local Similarity 88.7%; Pred. No. 2e-26; Indels 0; Gaps 0;
 Matches 94; Conservative 8; Mismatches 4;
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKFGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKFGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSGSGTEFTLTISLNQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
 DB 61 SGSGSGTEFTLTISLNQPEDFATYCCQOSYSTPTTFGQGTKEIKR 106
 RESULT 6
 AAG93590
 ID AAG93590 standard; protein; 107 AA.
 XX AAG93590;
 XX 14-SEP-2001 (first entry)
 DT Human anti-Rh(D) chain I02 protein sequence.
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 XX WFI; 2001-388931/41.
 DR N-PSDB; AAH68647.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Claim 1; Col 43; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX Sequence 107 AA;
 SQ Query Match 88.3%; Score 483; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 2.3e-26; Indels 0; Gaps 0;
 Matches 93; Conservative 10; Mismatches 3;
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKFGKAPKLLIWSASNLQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKFGKAPKLLIWSASNLQSGVPSRF 61
 QY 61 SGSGSGTEFTLTISLNQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
 DB 62 SGSGSGTEFTLTISLNQPEDFATYCCQOSYSTPTTFGQGTKEIKR 107
 RESULT 7
 ABO27397
 ID ABO27397 standard; protein; 107 AA.
 XX ABO27397;
 AC ABO27397;
 XX 12-SEP-2003 (first entry)
 DT Anti-Rh(D) chain I02.
 DE Human; RH(D) binding protein; blood typing; blood product; antibody;
 XX magnetically activated cell sorting.
 OS Homo sapiens.
 XX US2003040605-A1.
 PN 27-FEB-2003.
 PD 27-FEB-2003.
 XX


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PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45311.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 4; Page 26; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;
XX
Query Match 88.3%; Score 483; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.3e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVRTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTLTYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFTLTSSQLQPEDFATYCCQSYTLWTFGQTKVEIKR 107
RESULT 8
AAG93644
ID AAG93644 standard; protein; 107 AA.
XX
AC AAG93644;
XX
DT 14-SRP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH13 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
FN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAG68701.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

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PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 68; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;
XX
Query Match 87.8%; Score 480; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.8e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVRTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSRSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTLTYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFTLTSSQLQPEDFATYCCQSYTLTYTFGQTKLEIKR 107
RESULT 9
ABO27451
ID ABO27451 standard; protein; 107 AA.
XX
AC ABO27451;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH13.
XX
KW Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45365.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 4; Page 50; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,

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CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.8e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61

Qy 61 SGSGSGTEFTLTISNLFQFDPASYCQOSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITISSLPQDFPATYCCQSYSTPTTFQGGTKLEIKR 107

RESULT 10
ID AAR54261 standard; protein; 107 AA.
AC AAR54261;
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin light chain variable region b27.
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..21 /label= FR1
FT Region 22..33 /label= CDR1
FT Region 34..48 /label= FR2
FT Region 49..55 /label= CDR2
FT Region 56..87 /label= FR3
FT Region 88..95 /label= CDR3
FT Region 96..107 /label= FR4
XX
XX WO9407922-A1.
XX
XX 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 190; 248pp; English.
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The

CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAb regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54261
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.1e-26;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLFQFDPASYCQOSYTTLYTFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITISSLPQDFPATYCCQSYSTPTTFQGGTKLEIKR 106

RESULT 11
ID AAW01284 standard; protein; 107 AA.
AC AAW01284;
XX
XX 29-JAN-1997 (first entry)
DT
DE VL region of HIV neutralising MAb, clone b27.
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..21 /label= FR1
FT Region 22..32 /label= CDR1
FT Region 33..47 /label= FR2
FT Region 48..54 /label= CDR2
FT Region 55..86 /label= FR3
FT Region 87..95 /label= CDR3
FT Region 96..107 /label= FR4
XX
XX WO9602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.

XX The sequences given in AAW01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2 gene
 CC clone, b27. A MAB containing this VL sequence has the capacity to reduce
 CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. The MAB may be used for
 CC determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 XX
 XX Sequence 107 AA;
 SQ

Query Match 87.0%; Score 476; DB 2; Length 107;
 Best Local Similarity 87.7%; Pred. No. 7.1e-26;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSGSGTEFTLTISNLQFEDFASYVCOQSYTTLTYFGSGTKLEIKR 106
 DB 61 SGSGSGTDFTLTISLQPEDFATYVCOQSYSTPTQFGQTKLEIKR 106

RESULT 12
 AAY98245
 ID AAY98245 standard; protein; 107 AA.
 XX
 AC AAY98245;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Anti-gp120 antibody light chain variable region from clone B27.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048754.
 XX
 PR 16-SEP-1999; 99AU-00048754.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 2000-246867/22.
 DR
 PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 PS Example 9; Fig 11; 374pp; English.
 XX
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid

CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 XX Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;
 Best Local Similarity 87.7%; Pred. No. 7.1e-26;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSGSGTEFTLTISNLQFEDFASYVCOQSYTTLTYFGSGTKLEIKR 106
 DB 61 SGSGSGTDFTLTISLQPEDFATYVCOQSYSTPTQFGQTKLEIKR 106

RESULT 13
 AAY95136
 ID AAY95136 standard; protein; 107 AA.
 XX
 AC AAY95136;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Anti-gp120 antibody light chain variable region from clone B27.
 XX
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN AU9948756-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048756.
 XX
 PR 16-SEP-1999; 99AU-00048756.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 2000-293393/26.
 DR
 PT Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX
 PS Example 9; Fig 11; 366pp; English.
 XX

CC The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 CC
 CC Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;
 Best Local Similarity 87.7%; Pred. No. 7, 1e-26;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIYAASLSLQSGVPSRF 60
 Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTLYTFGSGTKLEIKR 106
 Db 61 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPTQFGGTKLEIKR 106

RESULT 14
 AAG93663
 ID AAG93663 standard; protein; 107 AA.
 AC AAG93663;
 XX
 XX 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH49 protein sequence.
 DE
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR N-PSDB; AAH68720.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Claim 1; Col 69; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;
 Best Local Similarity 85.8%; Pred. No. 8, 3e-26;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 2 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIYAASLSLQSGVPSRF 61
 Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTLYTFGSGTKLEIKR 106
 Db 62 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPTQFGGTKLEIKR 107

RESULT 15
 AAG93664
 ID AAG93664 standard; protein; 107 AA.

AC AAG93664;
 XX
 XX 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH50 protein sequence.
 DE
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR N-PSDB; AAH68720.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Claim 1; Col 69; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC

CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669, (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG68615 to AAG68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.3e-26;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ELTQSPSSLSASVGRVTITCRQSIITYLNWYQKFKGAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGRVTITCRQSIITYLNWYQKFKGAPKLLIWSASNLQSGVPSRF 61
Qy 61 SGSGSGTFTLTISNLFQEPFASYCQOSYTLTYFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISNLFQEPFASYCQOSYTLTYFGSGTKLEIKR 107

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Perfect score: 547
Sequence: 1 ELTQSPSSLASVGDRTVIT.....QQSYTLYTFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	100.0	106	14	US-10-027-725A-11
2	484	88.5	107	14	US-10-016-986-104
3	483	88.3	107	10	US-09-848-798-33
4	480	87.8	107	10	US-09-848-798-156
5	476	87.0	107	14	US-10-016-986-105
6	475	86.8	107	10	US-09-848-798-175
7	475	86.8	107	10	US-09-848-798-176
8	474	86.7	107	10	US-09-848-798-179
9	473.5	86.6	108	10	US-09-848-798-32
10	473.5	86.6	108	10	US-09-848-798-43
11	473	86.5	107	10	US-09-848-798-37
12	473	86.5	111	14	US-10-203-754A-57
13	472.5	86.4	108	10	US-09-848-798-167
14	472	86.3	107	10	US-09-848-798-38
15	472	86.3	107	10	US-09-848-798-39

16	472	86.3	107	10	US-09-848-798-162	Sequence 162, App
17	471	86.1	107	10	US-09-848-798-158	Sequence 158, App
18	469	85.7	107	10	US-09-848-798-44	Sequence 44, Appl
19	468	85.6	111	14	US-10-203-754A-56	Sequence 56, Appl
20	467	85.4	240	9	US-09-192-854-2	Sequence 2, Appli
21	467	85.4	240	9	US-09-968-561A-2	Sequence 2, Appli
22	467	85.4	240	10	US-09-968-744A-2	Sequence 2, Appli
23	467	85.4	240	12	US-09-968-561A-2	Sequence 2, Appli
24	466	85.2	107	10	US-09-791-153A-67	Sequence 67, Appl
25	465.5	85.1	107	12	US-10-460-595-9	Sequence 9, Appli
26	465	85.0	107	15	US-10-309-762-89	Sequence 89, Appl
27	464.5	84.9	108	10	US-09-848-798-163	Sequence 163, App
28	463	84.6	104	14	US-10-016-986-106	Sequence 106, App
29	463	84.6	107	15	US-10-309-762-88	Sequence 88, Appl
30	462	84.5	127	15	US-10-363-349-4	Sequence 4, Appli
31	460.5	84.2	107	12	US-10-363-349-4	Sequence 4, Appli
32	460.5	84.2	288	12	US-10-363-349-7	Sequence 7, Appli
33	460	84.1	106	14	US-10-027-725A-10	Sequence 10, Appl
34	459	83.9	107	10	US-09-848-798-168	Sequence 168, App
35	459	83.9	233	16	US-10-663-244-150	Sequence 150, App
36	458	83.7	106	15	US-10-377-121-5	Sequence 5, Appli
37	457	83.5	107	10	US-09-848-798-36	Sequence 36, Appl
38	457	83.5	214	14	US-10-153-382-19	Sequence 19, Appl
39	456.5	83.5	108	10	US-09-848-798-41	Sequence 41, Appl
40	456.5	83.5	108	14	US-10-016-986-109	Sequence 109, App
41	456	83.4	105	15	US-10-309-762-155	Sequence 155, App
42	456	83.4	107	10	US-09-848-798-173	Sequence 173, App
43	456	83.4	107	15	US-10-309-762-67	Sequence 67, Appl
44	456	83.4	107	15	US-10-309-762-68	Sequence 68, Appl
45	455	83.2	107	16	US-10-723-434-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-11

Query Match	100.0%	Score 547;	DB 14;	Length 106;
Best Local Similarity	100.0%	Pred. No. 1.2e-41;		
Matches 106;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	ELTQSPSSLASVGDRTVITTCRROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF	60	
Db	1	ELTQSPSSLASVGDRTVITTCRROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF	60	
QY	61	SGSGSGTEFTLTISNLQFEDFASYCQSYTYTLYTFGSGTKLEIKR	106	
Db	61	SGSGSGTEFTLTISNLQFEDFASYCQSYTYTLYTFGSGTKLEIKR	106	

RESULT 2

US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:

Be 3


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; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match
Best Local Similarity 87.0%; Score 476; DB 14; Length 107;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
Qy 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITSSLPQDFATYYCQOSYSTPTQTFGGTKVEIKR 106

RESULT 6
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match
Best Local Similarity 86.8%; Score 475; DB 10; Length 107;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQDFATYYCQOSYSTPTQTFGGTKVEIKR 107

RESULT 7
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-176

Query Match
Best Local Similarity 85.8%; Score 474; DB 10; Length 107;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQDFATYYCQOSYSTPTQTFGGTKVEIKR 107

RESULT 8
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match
Best Local Similarity 86.7%; Score 474; DB 10; Length 107;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQDFATYYCQOSYSTPTQTFGGTKVEIKR 107

RESULT 9
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.8e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPTPTFGGTRLEIKR 108

RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.8e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPTPTFGGTRLEIKR 108

RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.8e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPTPTFGGTRLEIKR 108

RESULT 12
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match      86.5%; Score 473; DB 14; Length 111;
Best Local Similarity 86.7%; Pred. No. 5.4e-35;
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 LTQSPSSLASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
Db 4 MTQSPSSLASVGDRTVITTCRASQRISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 63

Qy 62 SGSGSGTFTLTISNLQFEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 64 SGSGSGTFTLTISNLQFEDFATYCCQSYTPTPTFGGTRLEIKR 108

RESULT 13
US-09-848-798-167
; Sequence 167, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ; FILE REFERENCE: 09596-42U2
 ; CURRENT APPLICATION NUMBER: US/09/848,798
 ; CURRENT FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 167
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
 ; US-09-848-798-167

```

Query Match      86.4%; Score 472.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 5.9e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY      1 ELTQSPSSLASVGDRTVITICRAQSTISTYLNWYQQKPGKAPKLLINWSAGNLQSGVPSRF 60
         |||||
Db       2 ELTQSPSSLASVGDRTVITICRASQSTISSYLNWYQQKPGKAPKLLIYAASGLQSGVPSRF 61
         |||||

QY      61 SGGSGSGTFFLLTINLQDFEFASYVCOQSYTT-LYTFSGSGTKLEIKR 106
         |||||
Db       62 SGGSGSGDFFLTINSLQDFEFATYVCOQSYSTPTPTFGQGTKEIKR 108
         |||||

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RESULT 14

```

US-09-848-798-38
; Sequence 38, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-798-38

```

Query Match	86.3%	Score 472;	DB 10;	Length 107;
Best Local Similarity	86.8%;	Pred. No. 6.4e-35;		
Matches	92;	Conservative	9;	Mismatches 5; Indels 0; Gaps 0;
QY	1	ELTQSPSSLSASVGDRTVITTCRAPQSISTVILNWYQQKPGKAPKLLIWSASNLQSGVPSRF	60	
Db				
	2	ELTQSPSSLSASVGDRTVITTCRASQSISSYILNWYQQKPGKAPKLLIYAASLQSGVPSRF	61	
QY	61	SGSGSGTEPFLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR	106	
Db				
	62	SGSGSGTEPFLTISNLQPEDFAYYYCOOSYSTPRTFGGTVKIKR	107	

RESULT 15

US-09-848-798-39

```

; Sequence 39, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I08
US-09-848-798-39

Query Match      86.3%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 6,4e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY      1 ELTQPSLSASVGRVITTCRAQSISTYLNWYQQKPGKAPKLLIWSASNLQGVPSRF 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2 ELTQPSLSASVGRVITTCRASQISSYLNWYQQKPGKAPKLLIYAASSLQGVPSRF 61
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 SGSGSGTFTLLTISLQPEDFASYYCQSYTTLVTFGSGTKLEIKR 106
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      62 SGSGSGTFTLLTISLQPEDFATYYCQSYSTPRTFGGTKVEIKR 107
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: August 8, 2004, 12:43:21
Job time : 35.8152 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLASVGDRTIT.....QQSYTYLTFSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	88.5	107	1	US-08-276-852-104
2	484	88.5	107	1	US-08-899-575-104
3	484	88.5	107	1	US-08-899-575-104
4	484	88.5	107	5	PCT-US95-08743-104
5	483	88.3	107	3	US-09-240-274-33
6	480	87.8	107	3	US-09-240-274-156
7	476	87.0	107	1	US-08-276-852-105
8	476	87.0	107	1	US-08-899-575-105
9	476	87.0	107	1	US-08-899-575-105
10	476	87.0	107	5	PCT-US95-08743-105
11	475	86.8	107	3	US-09-240-274-175
12	475	86.8	107	3	US-09-240-274-176
13	474	86.7	107	3	US-09-240-274-179
14	473.5	86.6	108	3	US-09-240-274-32
15	473.5	86.6	108	3	US-09-240-274-43
16	473	86.4	107	3	US-09-240-274-37
17	472.5	86.4	108	3	US-09-240-274-167
18	472	86.3	107	3	US-09-240-274-38
19	472	86.3	107	3	US-09-240-274-39
20	472	86.3	107	3	US-09-240-274-162
21	471	86.1	107	3	US-09-240-274-158
22	469	85.7	107	3	US-09-240-274-44
23	468	85.6	108	2	US-08-379-057-29
24	464.5	84.9	108	3	US-09-240-274-163
25	463	84.6	104	1	US-08-276-852-106
26	463	84.6	104	1	US-08-899-575-106
27	463	84.6	104	1	US-08-899-575-106

ALIGNMENTS

RESULT 1

US-08-276-852-104

; Sequence 104, Application US/08276852

; Patent No. 5652138

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/276,852

; FILING DATE: 18-JUL-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: SCL452P

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 104:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-276-852-104

Sequence 106, App
Sequence 14, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 168, App
Sequence 66, Appl
Sequence 36, Appl
Sequence 3, Appl
Sequence 71, Appl
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 41, Appl
Sequence 109, App
Sequence 173, App
Sequence 103, App
Sequence 103, App
Sequence 103, App

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Query Match      88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.4e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
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Db 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
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RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.4e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-08-899-575-104
; Sequence 104, Application PC/TUS9508743
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QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
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Db 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
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RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.4e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNNWYQKPGKAPKLLIWAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTEFTLTISNLQFEDFASYCQOSYTTLYTFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
```

```

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BFO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      88.5%; Score 483; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-36;
Matches 94; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60

QY 61 SSGSGTFTLTISNLFQEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 61 SSGSGTDFLTITSLQLPEDFATYCCQSYSTPYTFGGQTKVEIKR 106

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.7e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

QY 61 SSGSGTFTLTISNLFQEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSLQLPEDFATYCCQSYSTPYTFGGQTKVEIKR 107
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```

RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.2e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

QY 61 SSGSGTFTLTISNLFQEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSLQLPEDFATYCCQSYSTPYTFGGQTKVEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652136
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRARQSIGISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTLTYFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITISSLOPEDFATYCOOSYSTPTQTFGGTKLEIKR 106

RESULT 8
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105
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; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRARQSIGISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTLTYFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITISSLOPEDFATYCOOSYSTPTQTFGGTKLEIKR 106

RESULT 9
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105
```



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Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYTTLTYTFSGKLEIKR 106
Db 61 SSGSGTFTLTISNLQPEDFATYCCQSYSTPQTGQGTKEIKR 106

RESULT 10
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match      87.0%; Score 476; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYTTLTYTFSGKLEIKR 106
Db 61 SSGSGTFTLTISNLQPEDFATYCCQSYSTPQTGQGTKEIKR 106

RESULT 11
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 9.1e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYTTLTYTFSGKLEIKR 106
Db 62 SSGSGTFTLTISNLQPEDFATYCCQSYSTPQTGQGTKEIKR 107

RESULT 12
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 9.1e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYTTLTYTFSGKLEIKR 106
Db 62 SSGSGTFTLTISNLQPEDFATYCCQSYSTPQTGQGTKEIKR 107

RESULT 13
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
```

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      86.6%; Score 473.5; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.1e-35;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSMSASVGDRTVITTCRAQSISGTILNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

Qy 61 SSGSGTFTLTISNLQFEDFASYCQOQSYTTLYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPTWTFGGIKVEIKR 107

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32
```

```
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

Qy 61 SSGSGTFTLTISNLQFEDFASYCQOQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQGTKEIKR 108

Search completed: August 8, 2004, 12:20:25
Job time : 13.6879 secs
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Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

Qy 61 SSGSGTFTLTISNLQFEDFASYCQOQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQGTKEIKR 108

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISSTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61

Qy 61 SSGSGTFTLTISNLQFEDFASYCQOQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQGTKEIKR 108

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 9.31515 Seconds
(without alignment)
1094.593 Million cell updates/sec

Title: US-10-027-725A-12
Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDRTVTIT.....QQANSFPYFGQGTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	84.2	117	2 S46376	Ig kappa chain V-J
2	462	84.2	125	2 S40316	Ig kappa chain - h
3	459	83.6	125	2 S40333	Ig kappa chain V-J
4	455	82.9	125	2 S40349	Ig kappa chain V-J
5	454.5	82.8	124	2 S40336	Ig kappa chain V-J
6	454	82.7	130	2 S40368	Ig kappa chain - h
7	451	82.1	128	2 S46372	Ig light chain var
8	451	82.1	131	2 S40352	Ig kappa chain V-J
9	450	82.0	105	2 S36266	Ig kappa chain V-J
10	447	81.4	127	2 S40367	Ig kappa chain V-J
11	446	81.2	108	2 S19674	Ig kappa chain V r
12	446	81.2	132	2 S38646	Ig kappa chain V r
13	445	81.1	117	2 S46371	Ig kappa chain V-J
14	444	80.9	123	2 S40331	Ig kappa chain - h
15	444	80.9	132	2 S40334	Ig kappa chain - h
16	443	80.7	108	2 S49047	Ig kappa chain V r
17	441	80.3	108	2 S47182	Ig kappa chain - h
18	441	80.3	109	2 S31998	Ig kappa chain - h
19	441	80.3	124	2 S40318	Ig kappa chain V r
20	439.5	80.1	108	2 S30521	Ig kappa chain V r
21	439	80.0	129	2 S40369	Ig kappa chain - h
22	437	79.6	107	2 S36264	Ig kappa chain V
23	435.5	79.3	108	2 S34007	Ig kappa chain V r
24	435	79.2	108	1 K1HUBN	Ig kappa chain V-I
25	434.5	79.1	107	2 S36275	Ig kappa chain V
26	434	79.1	108	1 K1HWS	Ig kappa chain V-I
27	434	79.1	108	2 S44122	Ig kappa chain V r
28	433	78.9	117	2 S21527	Ig kappa chain pre
29	432	78.7	108	2 S36283	Ig kappa chain V

ALIGNMENTS

RESULT 1

S46376

Ig kappa chain V-J region (T33-14) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

R:Accession: S46376; S38649

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46376

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27177; NID:G415969; PIDN:CAA81701.1; PID:G415970

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-99/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 117;
Best Local Similarity 84.9%; Pred. No. 2e-32; Mismatches 0; Gaps 0;
Matches 90; Conservative 7; Indels 9;

QY 1 ELTQSPSSVSASVGDRTVTITCRASQGISLAWYHQPKAPKLLIYASLSQSGVPSRF 60

Db ::|

12 QMTQSPSSVSASIGDRVTITCRASQDISLAWYQOKPGKAPKLLIYAASLSQSGVPLRF 71

QY 61 SSGSGYGTDFSLTISLSI-OFEDSATYTCQANSFPYFGQGTKVEIKR 106

Db ::|

72 SSGSGGTDFLTITSLQLPEDFATYTCQANSFPYFGQGTKVDIKR 117

RESULT 2

S40316

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

R:Accession: S40316

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40316

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72426

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 2.2e-32;

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Matches 91; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYHISSLTQGVPSRF 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SGSGSGTDFLTITISLQPEDFATYYCOQANSFPLTFGGTKVEIKR 123
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 459; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 3.9e-32;
Matches 87; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 QMTQSPSLASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYKASSLSQSGVPSRF 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKVEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGSGSGTEFTLTISLQPEDFATYYCOQYNSPYTFGGTKVEIK 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 455; DB 2; Length 125;
Best Local Similarity 84.9%; Pred. No. 8.5e-32;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QLTQSPSLASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYDASSLSQSGVPSRF 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SGSGSGTDFLTITISLQPEDFATYYCOQNTYPLTFGGTKVEIKR 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 454.5; DB 2; Length 124;
Best Local Similarity 84.1%; Pred. No. 9.3e-32;
Matches 90; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSLASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYAASTLQSGVPSRF 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SGSGSGTEFTLTISLQPEDFATYYCOQLNTYPTTFGGTKVEIKR 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S40368
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40368
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40368
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72478; NID:g441424; PIDN:CAA51146.1; PID:g441425
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 454; DB 2; Length 130;
Best Local Similarity 83.0%; Pred. No. 1.1e-31;
Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAHYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMTQSPSSVSASVGDRTVITCRASQDVAGWLAHYQHOPGKAPKLLIYAASTLQSEVPSRF 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SGSGSGTDFLTITISLQPEDFATYYCOQANSFPYTFGGTKVEIKR 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S46372
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46372
R:Ben Simon, C.; Chastagner, P.; Zouali, M.
```

EMBO J. 13, 2951-2962, 1994

A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46372
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <BEN>
A:Cross-references: EMBL:D27173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;
Best Local Similarity 83.0%; Pred. No. 1.9e-31;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQTSPSSVASVGDRTVTTCRASGGISSWLAWYOHGKAPKLLIYSASSLSQGVPSPRS 61
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
24 ITQSPSSLASAGTGRVTITCRASGGISSYLAWYQCKPGKAPKLLIYAASTLQSGVPSPRS 83
QY 62 GSGYGTDFTSLTISSLOFEDSATYYCCQANSFPYTFGGTKVEIKR 106
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 GSGSGTGDTFLTITSCLOSEDPATYYCQYYSYPRITFGGTKEIKR 128

RESULT 8

S40352
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40352
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40352
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;
Best Local Similarity 83.0%; Pred. No. 1.9e-31;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRVTITCRASGGISSWLAWYQHKGKAPKLLIYSASSLSQGVPSPRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
23 QMTQSPSSLASVGNRVTTITCRASGGISNYLAWYQCKPGKVPKLLIYAASSTLQSGVPSPRF 82
QY 61 SGSGYCTDFTSLTISSLOFEDSATYYCCQANSFPYTFGGTKVEIKR 106
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
83 GSGSGTGDTFLTITSCLOSEDPATYYCQYNSVPTFGGTKEIKR 128

RESULT 9

S36266
Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36266
R:Griffiths, A.D.; Malcolmist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36266
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-105 <GRI>
A:Cross-references: EMBL:Z18840; NID:g33423; PIDN:CAA79292.1; PID:g9939916
C:Superfamily: immunoglobulin V region; immunoglobulin homology

QY 62 GSGYGTDFSLTSSLOFEDSATYCCQANSFFYTFGGTKVEIKR 106
 Db 64 GSGSGTDFLTINSLOPEDFATYCCQOTNSFFLTFGGTKLEIKR 108

RESULT 12
 S38646
 Ig kappa chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C;Accession: S38646
 R;Bensimon, C.; Chastagner, P.; Zouali, M.
 submitted to the EMBL Data Library, November 1993
 A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A;Reference number: S38643
 A;Accession: S38646
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-132 <BEN>
 A;Cross-references: EMBL:Z27173; NID:g415961; PIDN:CAAB1697.1; PID:g415962
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;40-114/Domain: immunoglobulin homology <IMW>

Query Match 81.2%; Score 446; DB 2; Length 132;
 Best Local Similarity 82.9%; Pred. No. 5.1e-31;
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISLAWYQHQP KAPKLLIYASSSLSQGVPSRFS 61
 Db 28 IAGSPSSLASVGDRTVITTCRASQGLSSYLAWYQQK KAPKLLIYASTLSQGVPSRFS 87

QY 62 GSGYGTDFSLTSSLOFEDSATYCCQANSFFYTFGGTKVEIKR 106
 Db 88 GSGSGTDFLTITISLQSFEDFATYCCQYYSYPRTFGGTKVEIKR 132

RESULT 13
 S46371
 Ig kappa chain V-J region (T24-3) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C;Accession: S46371; S38645
 R;Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994
 A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene
 A;Reference number: S46369; GUID:94313975; PMID:8039491
 A;Accession: S46371
 A;Molecule type: mRNA
 A;Residues: 1-117 <BEN>
 A;Cross-references: EMBL:Z27172; NID:g415959; PIDN:CAAB1696.1; PID:g415960
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;23-97/Domain: immunoglobulin homology <IMW>

Query Match 81.1%; Score 445; DB 2; Length 117;
 Best Local Similarity 78.7%; Pred. No. 5.6e-31;
 Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLAWYQHQP KAPKLLIYASSSLSQGVPSRF 60
 Db 10 QMTQSFSTLSASVGDRTVITTCRASISITLAWYQQK KAPKLLIYKASTLDSGVPSRF 69

QY 61 GSGYGTDFSLTSSLOFEDSATYCCQANSF--FYTFGGTKVEIKR 106
 Db 70 GSGSGTDFLTITISLQPDDEFATYCCQYNSYFPYTFGGTKLEIKR 117

RESULT 14
 S40331
 Ig kappa chain - human
 C;Species: Homo sapiens (man)

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	435	79.2	108	1	KV1V HUMAN	P04430 homo sapien
2	434	79.1	108	1	KV1S HUMAN	P01611 homo sapien
3	426.5	77.7	107	1	KVID HUMAN	P01596 homo sapien
4	424	77.2	108	1	KV1R HUMAN	P01610 homo sapien
5	424	77.2	129	1	KV1W HUMAN	P04431 homo sapien
6	423	77.0	108	1	KV1G HUMAN	P01599 homo sapien
7	423	77.0	108	1	KV1J HUMAN	P01600 homo sapien
8	419	76.3	108	1	KV1F HUMAN	P01598 homo sapien
9	419	76.3	108	1	KV1L HUMAN	P01604 homo sapien
10	416	75.8	108	1	KV1O HUMAN	P01607 homo sapien
11	413	75.2	108	1	KV1B HUMAN	P01594 homo sapien
12	410	74.7	108	1	KV1M HUMAN	P01605 homo sapien
13	408	74.3	108	1	KV1E HUMAN	P01597 homo sapien
14	406	74.0	108	1	KV1A HUMAN	P01593 homo sapien
15	405	73.8	108	1	KV1P HUMAN	P01608 homo sapien
16	402	73.2	117	1	KV1I HUMAN	P01601 homo sapien
17	401	73.0	108	1	KV1N HUMAN	P01606 homo sapien
18	401	73.0	108	1	KV1J HUMAN	P03062 homo sapien
19	394	71.8	117	1	KV1J HUMAN	P01602 homo sapien
20	393	71.6	108	1	KV1C HUMAN	P01595 homo sapien
21	391	71.2	108	1	KV1K HUMAN	P01603 homo sapien
22	385	70.1	108	1	KV1Q HUMAN	P01609 homo sapien
23	385	70.1	129	1	KV1X HUMAN	P04432 homo sapien
24	383	69.8	108	1	KV5S MOUSE	P01652 mus musculu
25	380	69.2	108	1	KV5Q MOUSE	P01650 mus musculu
26	376	68.5	108	1	KV5T MOUSE	P01653 mus musculu
27	373	67.9	108	1	KV5K MOUSE	P01644 mus musculu
28	370.5	67.5	109	1	KV1T HUMAN	P01612 homo sapien
29	370	67.4	128	1	KV5E MOUSE	P01637 mus musculu
30	368	67.0	108	1	KV5L MOUSE	P01645 mus musculu
31	368	67.0	108	1	KV5O MOUSE	P01648 mus musculu
32	368	67.0	134	1	KV4C HUMAN	P06314 homo sapien
33	367.5	66.9	129	1	KV3M HUMAN	P18136 homo sapien

```

AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Wes.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01877; KIHUWS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B1A649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.4e-38;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQDISHLWAWYQQKSGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGSGVGTDFSLTISLQFDSATYYCOQANSFPYTFGGQTKVEIKR 106
DB 63 SGSGSGTFTLTISLQPEDFATYCCQAHSPVLPFGGGTTVDIKR 108

RESULT 3
KVLD HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region CAR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
```

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RL Eur. J. Biochem. 49:377-391 (1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR; A01864; KIHUAR.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 77.7%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.4e-37;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQDISHLWAWYQQKSGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGSGVGTDFSLTISLQFDSATYYCOQANSFPYTFGGQTKVEIKR 106
DB 63 SGSGSGTFTLTISLQPEDFATYCCQAHSPVLPFGGGTTVDIKR 107

RESULT 4
KVLR HUMAN STANDARD; PRT; 108 AA.
ID KVLR HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
```



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FT  DISULFID  23      88      BY SIMILARITY.
FT  NON TER   108      108
SQ  SEQUENCE  108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 108;
Matches 82; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY  1 ELTQSPSSVSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVPSRF 60
Db  3 QMTQSPSSLSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVTSRF 84

QY  61 SSGSGYTDFTSLTISSLQPEDSATYYCQANSFPYTFGGTKVEIKR 106
Db  63 SSGSGTEFTLTINSLQPEDFATYYCLOYSFRTFTGGTKVEIKR 108

RESULT 5
KVIG HUMAN STANDARD; PRT; 129 AA.
ID  KV1W HUMAN
AC  P04471
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-I region Walker precursor.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85014148; PubMed=6091049;
RA  Klobbeck H.G., Combriato G., Zachau H.G.;
RT  "Immunoglobulin genes of the kappa light chain type from two human
RL  lymphoid cell lines are closely related.";
RL  Nucleic Acids Res. 12:6995-7006(1984).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X00965; CAA25477.1; ALT_TERM.
DR  PIR; A01883; KIHUWK.
DR  HSSP; P01607; IREI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL  1 22
FT  CHAIN  23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT  DOMAIN  23 45 FRAMEWORK-1.
FT  DOMAIN  46 56 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN  57 71 FRAMEWORK-2.
FT  DOMAIN  72 78 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN  79 110 FRAMEWORK-3.
FT  DOMAIN  111 119 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN  120 129 FRAMEWORK-4.
FT  DISULFID  45 110
FT  NON TER  129 129 BY SIMILARITY.
SQ  SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 80.0%; Score 424; DB 1; Length 129;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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```

QY  1 ELTQSPSSVSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVPSRF 60
Db  25 QMTQSPSSLSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVTSRF 84

QY  61 SSGSGYTDFTSLTISSLQPEDSATYYCQANSFPYTFGGTKVEIKR 105
Db  85 SSGSGTDFTLTISLQPEDSATYYCQSYSTLTITFGGTRLEIKR 129

RESULT 6
KVIG HUMAN STANDARD; PRT; 108 AA.
ID  KV1G HUMAN
AC  P01599;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-I region Gal.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=75059122; PubMed=4215718;
RA  Laure C.J., Watanabe S., Hilschmann N.;
RT  "The primary structure of a monoclonal IgM-immunoglobulin
RL  (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT  kappa-type, subgroup I.";
RL  Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
CC  -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC  MACROGLOBULIN.
DR  PIR; A01867; KIHUGL.
DR  HSSP; P01607; IREI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN  1 23 FRAMEWORK-1.
FT  DOMAIN  24 34 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN  35 49 FRAMEWORK-2.
FT  DOMAIN  50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN  57 88 FRAMEWORK-3.
FT  DOMAIN  89 97 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN  98 107 FRAMEWORK-4.
FT  DISULFID  23 88 BY SIMILARITY.
FT  NON TER  108 108
SQ  SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match
Best Local Similarity 77.0%; Score 423; DB 1; Length 108;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY  1 ELTQSPSSVSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVPSRF 60
Db  3 QMTQSPSSLSASVGDRTVITCRASQGISWLAWYQHQPAPKLLIYASASSLSQGVTSRF 62

QY  61 SSGSGYTDFTSLTISSLQPEDSATYYCQANSFPYTFGGTKVEIKR 106
Db  63 SSGSGAGTEFTLTISLQPEDFATYYCLOQNSVPSRFGGTKVEIKR 108

RESULT 7
KV1H HUMAN STANDARD; PRT; 108 AA.
ID  KV1H HUMAN
AC  P01600;
DT  21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PTR; A01868; K1HUHU.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 77.0%; Score 423; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 3.4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVSGDRVTITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITCRASQSISSYLSWYQKPKAPQVLIYAASSLPQGVPSRF 62
Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGQTKVEIKR 106
Db 63 SGSGSGDTFTTISLQPEDFATYCCQNYITPTSFQGGTRVEIKR 108

RESULT 8
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.

21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE.
MEDLINE=71032830; PubMed=4097974;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
PTR; A01868; K1HUHU.
HSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
DOMAIN 1 23
DOMAIN 24 34
DOMAIN 35 49
DOMAIN 50 56
DOMAIN 57 88
DOMAIN 89 97
DOMAIN 98 107
DISULFID 23 88
NON TER 108 108
SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 77.0%; Score 423; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 3.4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVSGDRVTITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITCRASQSISSYLSWYQKPKAPQVLIYAASSLPQGVPSRF 62
Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGQTKVEIKR 106
Db 63 SGSGSGDTFTTISLQPEDFATYCCQNYITPTSFQGGTRVEIKR 108

RESULT 8
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
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RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PTR; A90562; K1HUEU.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.3%; Score 419; DB 1; Length 108;
Best Local Similarity 76.2%; Pred. No. 8.8e-37;
Matches 80; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVSGDRVTITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITCRASQSISSYLSWYQKPKAPKLLIYKASLESQGVPSRF 62
Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGQTKVEIK 105
Db 63 IGSGSGTEFTTISLQPEDFATYCCQYNSDSKMFQGGTKVEVK 107

RESULT 9
KVIL HUMAN
ID KVIL HUMAN STANDARD; PRT; 108 AA.
AC P01604.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PTR; A01870; K1HUKU.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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FT	DOMAIN	35	49	FRAMEWORK-2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	57	88	FRAMEWORK-3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	98	107	FRAMEWORK-4.
FT	DULFID	23	68	
FT	STRAND	4	7	
FT	STRAND	10	13	
FT	TURN	15	16	
FT	STRAND	19	25	
FT	TURN	30	31	
FT	STRAND	33	38	
FT	TURN	40	41	
FT	STRAND	44	49	
FT	TURN	50	52	
FT	STRAND	53	54	
FT	TURN	56	57	
FT	TURN	60	61	
FT	STRAND	62	67	
FT	TURN	68	69	
FT	STRAND	70	75	
FT	HELIX	80	82	
FT	STRAND	85	90	
FT	STRAND	97	98	
FT	STRAND	102	106	
FT	NON TER	108	108	
SQ	SEQUENCE	108 AA;	11902 MW;	9E8143E11898CE2A CRC64;

Query Match 75.8%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 1.8e-36;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps

QY	1	ELTQSPSSVSASVGDRTVITICRASQGISLAWVQHQPQKAPKLLIYSASSLSQSGVPSR
Db	3	QMTQSPSSLSASVGDRTVITICASQDIIRKYLNNWQQTGKAPKLLIYEASNQLQAGVPSR
QY	61	SGSGGTYDFTSLTISLQFDSATYICQANSFFYTTFGQTKVEIKR 106
Db	63	SGSGGTYDTFTISLQPEDIATYICQYOSLPYTFGQTKLQITR 108

RESULT 11

ID	KVIB HUMAN	STANDARD;	PRF;	108 AA.
AC	P01594;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain V-I region AU.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=72189444; PubMed=5028201;			
RA	Schlechl H., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal			
RT	immunoglobulin l-chain of the kappa-type, subgroup I (Bence-Jones			
RT	protein Au).";			
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY.			
RX	MEDLINE=77022433; PubMed=1234024;			
RA	Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,			
RA	Schwager P., Steigemann W., Schramm H.J.;			
RT	"The structure determination of the variable portion of the			
RT	Bence-Jones protein Au.";			
RL	Biophys. Struct. Mech. 1:139-146(1975).			
CC	!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY			
CC	MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V			
CC	REGION OF THE KAPPA CHAIN REI.			
CC	!- MISCELLANEOUS: THE C-REGION OF THIS CHAIN HAS THE SEQUENCE			

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91653; KIHU4U.
 DR PDB; 1JUV; 30-JAN-02.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR GO; GO:0007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 108 108
 FT NON TER 108
 FT SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 75.2%; Score 413; DB 1; Length 108;
 Best Local Similarity 75.5%; Pred. No. 3.7e-36;
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60
 DB 3 QMTQSPSSLSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 62
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 DB 63 SGSGSGAHTFTTISLQPEDATYCCQYDYLPLPWTFGGTKVEIKR 108

RESULT 12
 KWIM HUMAN
 ID KVIM HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Lay.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities.";
 RL Scand. J. Immunol. 5:677-684(1976)
 CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01871; KIHULY.
 DR HSSP; P01607; IREL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 108 108
 FT NON TER 108
 FT SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

FT DOMAIN 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 108 108
 FT NON TER 108
 FT SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 74.7%; Score 410; DB 1; Length 108;
 Best Local Similarity 72.6%; Pred. No. 7.6e-36;
 Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60
 DB 3 QMTQSPSSLSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 62
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 DB 63 SGSGSGTDFTTISLQPEDATYCCQYNNWPPTFGGTKVEIKR 108

RESULT 13
 KWIE HUMAN
 ID KWIE HUMAN STANDARD; PRT; 108 AA.
 AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RL Biochem. J. 123:945-958(1971)
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSSP; P01607; IREL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT 24 34
 FT 35 49
 FT 50 56
 FT 57 88
 FT 89 97
 FT 98 107
 FT 108 108
 FT NON TER 108
 FT SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 74.3%; Score 408; DB 1; Length 108;
 Best Local Similarity 72.6%; Pred. No. 1.2e-35;
 Matches 77; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60
 DB 3 ZMTQSPSSLSASVSGDRVTITCRAGQSVNKYLNWYQKPGKPKVLIFFAASSLSKSGVPSRF 62
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106

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Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 62
QY      61 SGGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGDTFTLTISLQPEDVATYCYKYNAPRTEPGTKLEIKR 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 4; Length 108;
Best Local Similarity 81.1%; Pred. No. 6.6e-40;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNVLAWYQKPGKPKAPNLLIYAASLTQSGVPSRF 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 SGGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGDTFTLTISLQPEDFATYCCQSYSTSWTFGGTKVEIKR 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 4; Length 108;
Best Local Similarity 81.1%; Pred. No. 6.6e-40;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNVLAWYQKPGKPKAPNLLIYAASLTQSGVPSRF 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 SGGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGDTFTLTISLQPEDFATYCCQSYSTSWTFGGTKVEIKR 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 77.7%; Score 426.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 9e-39;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNVLAWYQKPGKPKAPNLLIYAASLTQSGVPSRF 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 SGGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGDTFTLTISLQPEDFATYCCQSYSTSWTFGGTKVEIKR 107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 79.1%; Score 434; DB 4; Length 108;
Best Local Similarity 81.0%; Pred. No. 1.4e-39;
Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY      2 LTQSPSSVSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4 MTQSPSLLSASTGDRVTITSCRMSSQGISNVLAWYQKPGKAPPELLIYAASLTQSGVPSRF 63
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64 GSGSGGDTFTLTISLQPEDFATYCCQSYSTSWTFGGTKVEIKR 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes".
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 77.7%; Score 426.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 9e-39;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISNVLAWYQKPGKPKSLIYAASLTQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNVLAWYQKPGKPKAPNLLIYAASLTQSGVPSRF 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 SGGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGDTFTLTISLQPEDFATYCCQSYSTSWTFGGTKVEIKR 107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 5
Q72473
ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.6%; Score 426; DB 4; Length 234;
Best Local Similarity 78.1%; Pred. No. 2.7e-38;
Matches 82; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 61
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 MTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 83
QY 62 GSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 GSASGTDFTLISLQSEDFTATYTCQYKSPYTFGGTKVEIKR 128

RESULT 6
Q723Y4
ID Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.6%; Score 426; DB 4; Length 234;
Best Local Similarity 78.1%; Pred. No. 2.7e-38;
Matches 82; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 61
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 MTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 83
QY 62 GSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 GSASGTDFTLISLQSEDFTATYTCQYKSPYTFGGTKVEIKR 128

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RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 77.4%; Score 425; DB 4; Length 236;
Best Local Similarity 78.3%; Pred. No. 3.5e-38;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 QMTQSPSSVSASGVDRVTITCRASQIGISWLAHYQHPGKAPKLLIYSASSLOSQVPSRFS 84
QY 61 GSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGTKVEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 GSGSGGTDFTLITSLQSEDFTATYTCQYKSPYTFGGTKLEIKR 130

RESULT 7
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 -1

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FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.0%; Score 411.5; DB 4; Length 107;
Best Local Similarity 77.4%; Pred. No. 3.9e-37;
Matches 82; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 SGSGSGTDFLTISGLAQEDFATYCCQSVS-ALTFGPGIKVDIR 107

RESULT 8
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekkamoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR PDB; 1C1C; 11-NAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K6Q; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214 214
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 69.9%; Score 384; DB 11; Length 214;
Best Local Similarity 67.0%; Pred. No. 9.1e-34;
Matches 71; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QLTQSPSSVASYLGERVITTCASQDINSYLSWQPKGKSPKLLIYRANLVDGVPSRF 62

QY 61 SGSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 SGSGSGQDYSLTISLSEYDMGIYCYLQYDFEFPFTGSGTKLEIKR 108

RESULT 9
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWTLL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 69.6%; Score 382; DB 4; Length 108;
Best Local Similarity 65.7%; Pred. No. 6.5e-34;
Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 61
Db 4 MTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLIYCASTRATGIDARFS 63

QY 62 GSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 64 GSGSGTEFTLTSSLSQFEDFAVYCYQHYNNWPFPGTGVKDIKR 108

RESULT 10
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.W., Hong L.,
RA Datschenko L., Marusina K., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Toshikiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., McKernan K.J., Guarnatone P.H.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
```


Q8VJ0 Q8VJ00 PRELIMINARY; PRT; 108 AA.
AC Q8VJ00;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 66.7%; Score 366; DB 11; Length 108;
Best Local Similarity 64.8%; Pred. No. 3.6e-32;
Matches 68; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
QY 2 LTQSPSSVSASVGDRTVITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 61
DB 4 MTQSQTFMSTVSGDRSVTCKASQNVGTNVAWYQKPGQSPKALISASYPYSGVPHRT 63
QY 62 GSGYGTDFSLTISLQFEDSATYYCQANSFPYTFGGGTKVEIKR 106
DB 64 GSGSGTDFLTISNVQSEDLAEYFCQYNSYPYTFGGGTKLEIKR 108

RESULT 15
Q91WS9 Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 66.5%; Score 365; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 1.2e-31;
Matches 71; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60
DB 22 QMTQTTSLSASLGDRTVITCSGSGQGIANYLWYQKPGDGTVKLLIYYTSSLHSGVPSRF 81
QY 61 GSGYGTDFSLTISLQFEDSATYYCQANSFPYTFGGGTKVEIKR 106
DB 82 GSGSGTDFSLTISLQFEDSATYYCQANSFPYTFGGGTKLEIKR 127

Search completed: August 8, 2004, 12:17:47
Job time : 30.0697 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 43.5242 Seconds
(without alignments)
688.123 Million cell updates/sec

Title: US-10-027-725A-12
Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSPPYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	527	96.0	106	5	ABG30450 Human IGE
2	518	94.4	233	3	AA030713 Immunoglob
3	518	94.4	233	7	ADB72874 Human AAA
4	485	88.3	107	5	AB07237 Ant1-IL-4
5	484	88.2	223	6	ABJ36940 Anti-CD40
6	478	87.1	107	4	AAG65571 Amino aci
7	478	87.1	244	5	ABP45870 Human Bly
8	475	86.5	236	5	Aau74297 Anti-huma
9	474	86.3	105	5	AA018424
10	468	85.2	234	7	AD228413
11	467	85.1	107	4	AA072880 Human ant
12	467	85.1	134	6	ABR55899 Human mAb
13	466	84.9	108	5	AAU76522 Anti-Inte
14	466	84.9	234	7	AD228429 Human ant
15	464.5	84.6	109	4	AAE10815 Human ant
16	463	84.3	107	4	AA093597 Human ant
17	463	84.3	107	6	AB027404 Anti-Rh(D
18	463	84.3	107	7	AD228417 Human ant
19	462	84.2	107	4	AA072882 Human ant
20	462	84.2	224	4	AA075040 TRO005 Hu
21	461	84.0	107	7	AD228433 Human ant
22	461	84.0	132	6	ADA43065 Human ant
23	460	83.8	107	2	AA054260 Anti-HIV
24	460	83.8	107	2	AAW01283 VL region
25	460	83.8	107	3	AA098244 Anti-gp12

ALIGNMENTS

RESULT 1

ABG30450

ID ABG30450 standard; protein; 106 AA.

XX

AC ABG30450;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human IgE Fab clone 100 light chain protein.

XX

KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..21

FT Region /note= "FR1 region"

FT Region 22..32

FT Region /note= "CDR1 region"

FT Region 33..47

FT Region /note= "FR2 region"

FT Region 48..54

FT Region /note= "CDR2 protein"

FT Region 55..86

FT Region /note= "FR3 region"

FT Misc-difference 65

FT Region /note= "Encoded by TCT"

FT Region 87..95

FT Region /note= "CDR2 region"

FT Region 96..104

FT Region /note= "FR4 region"

XX

PN WO200253595-A1.

XX

XX 11-JUL-2002.

XX

XX 27-DEC-2001; 2001WO-SE002908.

XX

XX 29-DEC-2000; 2000SE-00004892.

XX

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX

PI Flicker S, Steinberger P, Kraft D, Valenta R;

XX

XX WPI; 2002-583e04/62.

XX

XX N-PSDB; ABK89642.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 41; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
 CC antibodies to phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergenic patients
 CC IgE antibodies to phi p 2. The present sequence represents the human IgG
 CC fab, clone 100 light chain protein of the invention

XX Sequence 106 AA;

Query Match 96.0%; Score 527; DB 5; Length 106;
 Best Local Similarity 97.2%; Pred. No. 5.1e-30;
 Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
 DB 1 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60

QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106
 DB 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106

RESULT 2
 AAB03713
 ID AAB03713 standard; protein; 233 AA.

XX AAB03713;

DT 04-OCT-2000 (first entry)

XX Immunoglobulin kappa amino acid sequence fragment.

XX Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
 KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
 KW immunoglobulin kappa; Igk.

XX Unidentified.

XX USG048704-A.

XX 11-APR-2000.

XX 07-MAR-1997; 97US-00812586.

XX 07-MAR-1996; 96US-0012976P.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Tilson MD;

XX WPI; 2000-316895/27.

XX Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
 PT disease is purified from human aortic tissue and binds immunoreactively
 PT with immunoglobulin.

PS Example 3; Col 29-31; 70pp; English.

XX The present invention relates to an isolated microfibrillar protein of
 CC approximately 40kD. The protein is isolated from human aortic tissue and
 CC binds immunoreactively with immunoglobulin purified from human abdominal
 CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
 CC aneurysm-associated antigenic protein (AAP). The protein is capable of
 CC forming a disulphide bonded dimer. The protein is immunoreactive with
 CC human kappa immunoglobulin. Also included in the invention are
 CC recombinantly produced human AAA proteins. AAP shows regions of homology
 CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
 CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
 CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
 CC presence of AAA-associated immunoglobulin bound to the human aortic
 CC tissue. Antibodies directed against AAP can be used to detect AAA
 CC disease. The recombinant protein can be used to induce tolerance to
 CC antigenic AAA protein in the subject e.g. human. This sequence represents
 CC an immunoglobulin kappa amino acid sequence. The sequence shares homology
 CC with the AAP of the invention, it was used to identify and characterise
 CC AAP

XX Sequence 233 AA;

Query Match 94.4%; Score 518; DB 3; Length 233;
 Best Local Similarity 96.2%; Pred. No. 4.4e-29;
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
 DB 23 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 82

QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106
 DB 83 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 128

RESULT 3
 ADB72874
 ID ADB72874 standard; protein; 233 AA.

XX ADB72874;

XX 04-DEC-2003 (first entry)

XX Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.

XX Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;

XX AAA-associated immunoglobulin 40kDa protein.

XX Homo sapiens.

XX USG537769-B1.

XX 25-MAR-2003.

XX 28-MAR-2000; 2000US-00535832.

XX 07-MAR-1996; 96US-0012976P.

XX 07-MAR-1997; 97US-00812586.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Tilson MD;

XX WPI; 2003-687181/65.

XX Purified protein useful in diagnosing abdominal aortic aneurysm disease
 PT in subject, e.g. human, contains specified amino acids.

XX Disclosure; Col 73-74; 67pp; English.

XX The present invention relates to the isolation of a protein approximately
 CC 40kDa which is purified from human aortic tissue. The protein is
 CC immunoreactive with abdominal aortic aneurysms (AAA)-associated

CC immunoglobulin. The protein is useful for diagnosing AAA disease in a
 CC subject, e.g. human, by administering the protein or a composition
 CC comprising the protein. The inventive protein is capable of forming a
 CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown
 CC function is given in the Sequence Listing but is not mentioned elsewhere
 CC in the specification.

XX SQ Sequence 233 AA;

Query Match 94.4%; Score 518; DB 7; Length 233;
 Best Local Similarity 96.2%; Pred. No. 4.4e-29;
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 60

DB 23 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 82

QY 61 SGSGYGTDFSLTITSSLOPDSATYYCQANSFPYTFQGTKEIKR 106

DB 83 SGSGSGTDFSLTITSSLOPDSATYYCQANSFPYTFQGTKEIKR 128

RESULT 4

ABB07237
 ID ABB07237 standard; protein; 107 AA.

AC ABB07237;

XX 26-MAR-2002 (first entry)

DE Anti-IL-4 and IL-13 receptors MAb 63 light chain variable region.

XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
 KW antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;
 KW antischlicking; immunosuppressive; tuberculostatic; ophthalmological;
 XX IL-13; antianemic; antithyroid.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 24..34
 /note= "complementarity determining region (CDR) 1"

FT Region 50..56
 /note= "complementarity determining region (CDR) 2"

FT Region 89..97
 /note= "complementarity determining region (CDR) 3"

XX WO200192340-A2.

PD 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US017094.

XX 26-MAY-2000; 2000US-00579808.

PR 19-SEP-2000; 2000US-0065343.

PR 15-FEB-2001; 2001US-00785934.

XX 01-MAY-2001; 2001US-00847816.

XX (IMV) IMMUNEX CORP.

XX Plueneke JD;

XX WPI; 2002-114332/15.

DR N-PSDB; ABA94337.

XX Novel human antibody which binds human interleukin (IL)-4 receptor and is
 PT capable of inhibiting IL-4 induced biological activity, functions as IL-4
 PT antagonist and is useful for treating septic arthritis, scleroderma.

XX Claim 3; Page 82; 85pp; English.

XX The invention relates to a human antibody (an interleukin (IL)-4

CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for
 CC inhibiting both IL-4-induced biological activity and IL-13-induced
 CC biological activity in vivo in a human, and for treating septic arthritis
 CC in a human afflicted with septic arthritis. (I) is also used for treating
 CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
 CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
 CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
 CC inflammatory bowel disease, other disorders of the digestive system in
 CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
 CC gastrointestinal tract), conditions in which IL-4-induced barrier
 CC disruption plays a role (e.g. conditions characterized by decreased
 CC epithelial barrier function in the lung or gastrointestinal tract),
 CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostate
 CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
 CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
 CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
 CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
 CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
 CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
 CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
 CC antagonists also find use as adjuvants to allergy immunotherapy and as
 CC vaccine adjuvants, especially when directing the immune response toward a
 CC TH1 response would be beneficial in treating or preventing the disease.
 CC The present sequence represents an anti-IL-4 receptor and anti-IL-13
 CC receptor monoclonal antibody (MAb) 63 light chain variable region
 XX Sequence 107 AA;

Query Match 88.3%; Score 485; DB 5; Length 107;
 Best Local Similarity 88.6%; Pred. No. 4.6e-27;
 Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 60

DB 3 QMTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 62

QY 61 SGSGYGTDFSLTITSSLOPDSATYYCQANSFPYTFQGTKEIK 105

DB 63 SGSGSGTDFSLTITSSLOPDSATYYCQANSFPYTFQGTKEIK 107

RESULT 5

ABJ36940

ID ABJ36940 standard; protein; 223 AA.

XX AC ABJ36940;

XX 01-MAY-2003 (first entry)

DE Anti-CD40 monoclonal antibody related protein SEQ ID No 66.

XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
 KW dendritic cell; high G28-5; CD55 expression; high G28-5; B cell line;
 KW immunoactivator; anti-tumour agent; immunosuppressant; allergy;
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.

OS Unidentified.

XX WO200288186-A1.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-JP004292.

XX 27-APR-2001; 2001WO-US013672.

PR 11-MAY-2001; 2001JP-0042482.

PR 05-OCT-2001; 2001JP-00310535.

XX 26-OCT-2001; 2001US-00040244.

XX (KIRI) KIRIN BEER KK.

XX Miyayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX WPI; 2003-120463/11.
 DR N-PSDB; ABT31882.
 XX
 PT Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
 PT or functional fragment, is useful in the treatment of e.g. autoimmune
 PT diseases or cancer.
 XX
 XX Claim 15; Page 60; 94pp; Japanese.
 XX
 XX The invention relates to an antibody to human CD40, or its functional
 CC fragment, has at least one of the following properties: acting on
 CC dendritic cells to produce IL-12 in the presence of LPS
 CC (lipopolysaccharide) and IFN γ (interferon gamma); acting on dendritic
 CC cells to activate maturation of the dendritic cells with high G28-5
 CC antibody; and activating CD95 expression with high G28-5 antibody against
 CC B cell line. Such antibodies or functional fragments can be used as
 CC immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies
 CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
 CC syndrome. This sequence represents a protein relating to the anti-CD40
 CC monoclonal antibody of the invention
 XX
 SQ Sequence 223 AA;

Query Match 88.2%; Score 484; DB 6; Length 223;
 Best Local Similarity 87.7%; Pred. No. 1e-26; Indels 0; Gaps 0;
 Matches 93; Conservative 7; Mismatches 6;
 Qy 1 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
 Db 25 QMTQSPSSVSASVGDRTVITICRASQGISLWAWYQHOPGKAPKLLIYAGSLQSGVPSRF 84
 Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106
 Db 85 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 130

RESULT 6
 AAG65571
 ID AAG65571 standard; protein; 107 AA.
 AC AAG65571;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of protein seq Id No. 96.
 XX
 KW Gene library; immunoglobulin; antibody library; human.
 XX
 OS Homo sapiens.
 XX
 FN WO200162907-A1.
 XX
 PD 30-AUG-2001.
 XX
 PF 22-FEB-2001; 2001WO-JP001298.
 XX
 PR 22-FEB-2000; 2000JP-00050543.
 XX
 PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 XX
 PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
 FI Okuno Y, Shiraki K;
 XX
 DR WPI; 2001-565420/63.
 DR N-PSDB; AAH47735.
 XX
 XX Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions.
 XX
 XX Examples; p 172; 181pp; Japanese.
 PS

XX The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries
 XX
 SQ Sequence 107 AA;

Query Match 87.1%; Score 478; DB 4; Length 107;
 Best Local Similarity 86.6%; Pred. No. 1.4e-26;
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSVSASVGDRTVITICRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTVITICRASQGISLWAWYQHOPGKAPKLLIYAGSLQSGVPSRF 62
 Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIK 105
 Db 63 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIK 107

RESULT 7
 ABP45870
 ID ABP45870 standard; protein; 244 AA.
 AC ABP45870;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1881.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 FN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUNA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 PT
 PS Claim 1; Page 2646-2647; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). BAP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX Sequence 244 AA;
 SQ

Query Match 87.1%; Score 478; DB 5; Length 244;
 Best Local Similarity 88.6%; Pred. No. 3e-26;
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 2 LTQSPSSVSASVGDRTVTTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 61
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 140 MTQSPSTLSASVGDRTVTTCRASQGISLWAWYQKPGKAPKLLIYAASSLSQSGVPSRF 199
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 62 GSGYGTDFSLTSSIQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 200 GSGSGTDFLTITSSIQPEDFATYCCQANSFPLTFGGTKVEIKR 244

RESULT 8
 ID AAU74297
 XX AAU74297 standard; protein; 236 AA.
 AC AAU74297;
 DT 12-MAR-2002 (first entry)
 XX
 DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.
 XX
 DE Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotrophic;
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KW systemic lupus erythematosus; autoimmune disorder; inflammation;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 XX
 OS Homo sapiens.
 XX WO200187981-A2.
 PN
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-JP004035.
 XX
 PR 18-MAY-2000; 2000JP-00147116.
 PR 30-MAR-2003; 2001JP-00099508.
 XX
 XX (NISB) JAPAN TOBACCO INC.
 PA
 XX Tsuji T, Tezuka K, Hori N;
 XX WPI; 2002-075313/10.
 DR N-PSDB; AAS99473.
 DR
 XX New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule; useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation.
 XX
 PS Claim 30; Page 270-271; 300pp; English.
 XX
 CC The invention relates to a novel human antibody (I), preferably a human

CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AILIM, for modulating proliferation
 CC of AILIM-expressing cells, for modulating production of a cytokine from
 CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AILIM-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AILIM-mediated costimulatory
 CC transduction, and for inhibiting the onset and/or advancement of the
 CC diseases. (I) is useful for suppression, prevention and/or treatment of
 CC rheumatoid arthritis, multiple sclerosis, chronic inflammatory dermatitis,
 CC allergic contact-type dermatitis, insulin-dependent diabetes mellitus,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
 CC host reaction, graft versus host disease, immune rejection, disorders
 CC caused by abnormal intestinal immunity, specifically inflammatory
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
 CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
 CC AILIM monoclonal antibody amino acid sequences of the invention
 XX
 SQ Sequence 236 AA;

Query Match 86.5%; Score 475; DB 5; Length 236;
 Best Local Similarity 88.7%; Pred. No. 4.7e-26;
 Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVGDRTVTTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 25 QMTQSPSSVSASVGDRTVTTCRASQGISLWAWYQKPGKAPKLLIYVASSLSQSGVPSRF 84
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 GSGYGTDFSLTSSIQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 85 GSGSGTDFLTITSSIQPEDFATYCCQANSFPLTFGGTKVEIKR 130

RESULT 9
 ID AA018424
 XX AA018424 standard; protein; 105 AA.
 AC AA018424;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Anti-GD2 antibody light chain #1.
 KW
 KW Anti-GD2 antibody; neuroectodermal tumour; cancer; neuroblastoma;
 KW melanoma; vaccine; gene therapy; cytostatic; disialoganglioside GD2.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN DE10059930-A1.
 XX
 PD 29-MAY-2002.
 XX
 PF 23-NOV-2000; 2000DE-01059930.
 XX
 PR 23-NOV-2000; 2000DE-01059930.
 XX
 XX (FISC/) FISCHER P.
 PA (UTTE/) UTTEBREUTHER-FISCHER M.
 XX
 XX Uttenreuther-Fischer M, Krueger J;
 XX WPI; 2002-510006/55.
 DR
 XX Composition for treating tumors that produce disialoganglioside GD2,
 PT comprises human antibody fragment able to induce anti-idiotypic
 PT antibodies.
 XX

PS Claim 3; Fig 7A; 14pp; German.
 XX
 CC The present invention relates to a composition for treating tumours
 CC positive for disialoganglioside GD2 which is based on human antibody
 CC fragments that activate the immune system against GD2, specifically by
 CC inducing anti-GD2 antibodies. The composition can be used in the
 CC treatment of neuroblastoma and melanoma. The present sequence is an anti-
 CC GD2 antibody light chain
 XX
 SQ Sequence 105 AA;
 Query Match 86.3%; Score 474; DB 5; Length 105;
 Best Local Similarity 89.5%; Pred. No. 2.7e-26;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60
 Db 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASLSQSGVPSRF 60
 Qy 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPYTFQGTKEIKR 105
 Db 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPYTFQGTKEIKR 105
 Db 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPYTFQGTKEIKR 105
 RESULT 10
 ADE28413
 ID ADE28413 standard; protein; 234 AA.
 XX
 AC ADE28413;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human anti-CD40 antibody 10-8-3 variable region light chain protein.
 XX
 KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region light chain; 10-8-3.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040170-A2.
 XX
 PD 15-MAY-2003.
 XX
 PP 08-NOV-2002; 2002WO-US036107.
 XX
 PR 09-NOV-2001; 2001US-0348980P.
 XX
 PA (PFIZ) PFIZER PROD INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX
 DR WPI; 2003-441521/41.
 DR N-PSDB; ADE28412.
 XX
 PT New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 XX
 PS Claim 1; SEQ ID NO 20; 177pp; English.
 XX
 CC The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region light chain protein of the invention.
 XX
 SQ Sequence 234 AA;
 Query Match 85.2%; Score 468; DB 7; Length 234;
 Best Local Similarity 86.8%; Pred. No. 1.4e-25;
 Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60
 Db 23 QMTQSPSSVSASVGDRTVITTCRASQPTISSWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 82
 Qy 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPYTFQGTKEIKR 106
 Db 83 SGSGYGTDFSLTISLQFDSATYCCOANSFPYTFQGTKEIKR 128
 RESULT 11
 AAB72880
 ID AAB72880 standard; protein; 107 AA.
 XX
 AC AAB72880;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Human anti-HER2/neu antibody 3-F2 light chain.
 XX
 KW Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
 KW 1-D2; 2-E8; growth factor receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200109187-A2.
 XX
 PD 08-FEB-2001.
 XX
 PP 25-JUL-2000; 2000WO-US020272.
 XX
 PR 29-JUL-1999; 99US-0146313P.
 PR 10-MAR-2000; 2000US-0188539P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Keler T, Deo Y;
 XX
 DR WPI; 2001-168698/17.
 DR N-PSDB; AAF75586.
 XX
 PT New human monoclonal antibody that specifically binds to growth factor
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases
 PT characterized by aberrant HER2/neu expression e.g. cancers.
 XX
 PS Disclosure; Page 104-105; 113pp; English.
 XX
 CC The present invention provides the protein and coding sequences for human
 CC monoclonal antibodies which bind specifically to the HER2/neu growth
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
 CC and 2-E8. They can be used in the immunotherapy-based treatment and
 CC prognosis of cancers, particularly adenocarcinomas such as salivary
 CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
 CC and ovarian cancer. The present sequence is part of an antibody of the
 CC invention
 XX
 SQ Sequence 107 AA;
 Query Match 85.1%; Score 467; DB 4; Length 107;
 Best Local Similarity 85.7%; Pred. No. 8.5e-26;
 Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASLSQSGVPSRF 62

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCQANSFYTFGQGTKEIK 105
Db 63 SSGSGIDFTLTISLQFEDFATYCCQANSFYTFGQGTKEIK 107

RESULT 12

ABR55899
ID ABR55899 standard; protein; 134 AA.

XX AC ABR55899;
XX DT 02-SEP-2003 (first entry)
XX DE Human mAb 4C2 light chain VJ region.

XX KW Mitochondrial antigen; autoantibody; biliary cirrhosis; transgenic;
XX KW monoclonal antibody; mAb.

XX OS Homo sapiens.

XX PN WO200276406-A2.

XX PD 03-OCT-2002.

XX XX 27-MAR-2002; 2002WO-US009694.

XX PF 27-WAR-2001; 2001US-0279052P.

XX PR 21-SEP-2001; 2001US-0323920P.

XX PA (GERS/) GERSHWIN M E.

XX PI Gershwin ME;

XX XX WPI; 2003-018951/01.

XX PT New anti-mitochondrial antigen specific human monoclonal antibodies from
XX PT patients with primary biliary cirrhosis (PBC), useful as a diagnostic
XX PT reagent, or as a reagent for screening antagonists for treating patients
XX PT with PBC.

XX PS Claim 22; Page 102; 150pp; English.

XX CC The invention relates to an isolated human antibody or its antigen-
XX CC binding portions, which binds a mitochondrial antigen bound by a human
XX CC autoantibody found in patients with primary biliary cirrhosis. The
XX CC antibody is useful as a diagnostic reagent, e.g. for monitoring whether a
XX CC transplanted liver in a patient with primary biliary cirrhosis, is
XX CC expressing a mitochondrial antigen bound by an autoantibody. The antibody
XX CC is also useful for purifying an antigen to which it binds, for producing
XX CC an anti-idiotypic antibody to it, or as a reagent to screen for
XX CC antagonists to it, either in vivo or in vitro. The antagonist is useful
XX CC for treating a patient with primary biliary cirrhosis, or for
XX CC prophylactically treating a patient about to have primary biliary
XX CC cirrhosis. The present sequence represents the VJ region of the light
XX CC chain of an anti-mitochondrial antigen human mAb (monoclonal antibody)
XX CC 4C2

XX SQ Sequence 134 AA;

Query Match 85.1%; Score 467; DB 6; Length 134;
Best Local Similarity 87.4%; Pred. No. 1e-25;
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 QSPSSVSASGDRVTITCRASGIGSSWLAWYQHPGKAPKLLIYASASSLQSGVPSRFGS 63

Db 1 QSPSSVSASGDRVTITCRASGIGSSWLAWYQHPGKAPKLLIYASASSLQSGVPSRFGS 60

QY 64 GYCTDFSLTISLQFEDSATYCCQANSFYTFGQGTKEIKR 106

Db 61 GSGTDFLTISLQFEDFATYCCQANSFYTFGQGTKEIKR 103

RESULT 13

AAU76522
ID AAU76522 standard; protein; 108 AA.

XX AC AAU76522;

XX DT 05-JUN-2002 (first entry)

XX DE Anti-Interleukin-12 (IL-12) antibody variable region #2.

XX KW Human; antibody; anti-interleukin-12; CDR; heavy chain; circulatory;
XX KW complementarity determining region; neuroprotective; antipsoriatic;
XX KW immunostimulant; cytostatic; anti-microbial; psoriasis; infection;
XX KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
XX KW neurological disorder.

XX OS Homo sapiens.

XX PN WO200212500-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024720.

XX PR 07-AUG-2000; 2000US-0223358P.

XX PR 29-SEP-2000; 2000US-0236827P.

XX PR 01-AUG-2001; 2001US-00920262.

XX PA (CENZ) CENTOCOR INC.

XX PI Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;

XX XX WPI; 2002-257482/30.

XX PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL
XX PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as
XX PT other for treating immune, infectious, malignant or neurological
XX PT disorders.

XX PS Claim 1; Page 93-94; 96pp; English.

XX CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL
XX CC -12) antibodies. The antibodies comprise at least one complementarity
XX CC determining region (CDR) of a heavy or light chain, a heavy chain or
XX CC light chain variable region, or a heavy chain or light chain constant
XX CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
XX CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
XX CC The antibodies are also useful for treating immune, cardiovascular,
XX CC infectious, malignant or neurological disorders or diseases. The present
XX CC sequence represents the amino acid sequence of human anti-interleukin-12
XX CC (IL-12) antibody variable region #2

XX SQ Sequence 108 AA;

Query Match 84.9%; Score 466; DB 5; Length 108;
Best Local Similarity 84.9%; Pred. No. 1e-25;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASGDRVTITCRASGIGSSWLAWYQHPGKAPKLLIYASASSLQSGVPSRF 60

Db 3 QMTQSPSSLSASGDRVTITCRASGIGSSWLAWYQHPGKAPKLLIYASASSLQSGVPSRF 62

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCQANSFYTFGQGTKEIKR 106

Db 63 SSGSGTDFLTISLQFEDFATYCCQVNIYPYTFGQGTKEIKR 108

RESULT 14

ADE28429
ID ADE28429 standard; protein; 234 AA.

XX AC ADE28429;

DT 29-JAN-2004 (first entry)
 XX Human anti-CD40 antibody 21-2-1 variable region light chain protein.
 XX
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human, variable region light chain; 21-2-1.
 XX
 OS Homo sapiens.
 XX
 XX WO2003040170-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 08-NOV-2002; 2002WO-US036107.
 XX
 XX 09-NOV-2001; 2001US-0348980P.
 XX
 XX (PFIZ) PFIZER PROD INC.
 XX (ABGE-) ABGENIX INC.
 XX
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX
 XX WPI; 2003-441521/41.
 XX N-PSDB; ADE28428.
 XX
 XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 XX
 XX Claim 1; SEQ ID NO 36; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region light chain protein of the invention.

XX Sequence 234 AA;

Query Match 84.9%; Score 466; DB 7; Length 234;
 Best Local Similarity 85.8%; Pred. No. 2e-25;
 Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTTTCRASQGISSWLAWYQHOPGKAPKLLIYASASLQSGVPSRF 60
 Db 23 QMTQSPSSVASVGDRTTTCRASQGISSWLAWYQKPGKAPNLIYASTLQSGVPSRF 82
 Qy 61 SGSGYGTDFSLTITSSLOFEDSATYCCOANSFPYTFGGTKVEIKR 106
 Db 83 SGSGSGTDFTLTITSSLOPEDFATYCCOANIFPLTFGGTKVEIKR 128

RESULT 15

AAE10815
 ID AAE10815 standard; protein; 109 AA.

XX AAE10815;

XX 18-DEC-2001 (first entry)

XX Human antibody CAT-212 light chain variable domain.

XX Human; eotaxin; CAT-212; antibody; light chain variable region; VL;
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;

KW vasotropic; conjunctivitis; allergic colitis; psoriasis; pemphigoid;
 KW eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;
 KW inflammatory bowel disease; gastroenteritis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..2 /note= "Encoded by ACATC"
 FT
 FT
 XX
 XX WO200166754-A1.
 XX
 XX 13-SEP-2001.
 XX
 XX 02-MAR-2001; 2001WO-GB000927.
 XX
 XX 03-MAR-2000; 2000US-0187246P.
 XX
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Vaughan TJ, Wilton AJ, Smith S;
 XX
 XX WPI; 2001-589944/66.
 XX N-PSDB; AAD18149.

Human antibodies against eotaxin useful for treating asthma, eczema and
 other atopic diseases, comprises an antibody variable heavy or variable
 PT light domain from CAT-212 or from complementary determining regions.

XX Claim 1; Page 102; 107pp; English.

XX The invention relates to a specific binding member which binds to human
 CC eotaxin. The binding member comprises an antibody variable heavy
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL
 CC domain comprising one or more VH/VL complementary determining regions
 CC (CDRs). Eotaxin is a chemoattractant protein that binds to a specific
 CC receptor which is expressed predominantly on eosinophils. The binding
 CC member is useful for neutralising eotaxin, which is useful in treating
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-
 CC mediated diseases; for treating skin and other atopic conditions such as
 CC psoriasis, pemphigoid, wells' syndrome, cellulitis, drug eruptions;
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin
 CC syndrome, Churg-Strassman syndrome. The present sequence is human antibody
 CC CAT-212 light chain variable domain (VL) which binds to eotaxin

XX Sequence 109 AA;

Query Match 84.6%; Score 464.5; DB 4; Length 109;
 Best Local Similarity 86.0%; Pred. No. 1.3e-25;
 Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy 1 ELTQSPSSVASVGDRTTTCRASQGISSWLAWYQHOPGKAPKLLIYASASLQSGVPSRF 60
 Db 3 QMTQSPSSVASVGDRTTTCRASQGISSWLAWYQKPGKAPKLLIYAAASLQSGVPSRF 62
 Qy 61 SGSGYGTDFSLTITSSLOFEDSATYCCOANSFP-YTFGGTKVEIKR 106
 Db 63 SGSGSGTDFTLTITSSLOPEDFATYCCOANSFPITFGGTRLEIKR 109

Search completed: August 8, 2004, 12:13:50
 Job time : 45.5242 secs

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OM protein - protein search, using sw model

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Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPYTFGGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

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Maximum Match 100%

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	106	14	US-10-027-725A-12
2	484	88.2	223	16	US-10-693-629-66
3	482	87.8	107	15	US-10-309-762-159
4	481	87.6	107	12	US-10-292-088-105
5	479	87.2	107	15	US-10-309-762-62
6	479	87.2	107	15	US-10-309-762-164
7	478	87.1	107	15	US-10-309-762-61
8	478	87.1	107	15	US-10-309-762-64
9	478	87.1	244	10	US-09-880-748-1881
10	478	87.1	244	12	US-10-293-418-1881
11	475	86.5	236	9	US-09-859-053-30
12	474	86.3	107	14	US-10-041-860-43
13	474	86.3	107	14	US-10-041-860-218
14	474	86.3	107	16	US-10-665-383-64
15	473.5	86.2	106	15	US-10-309-762-84

16	472	86.0	107	15	US-10-309-762-60	Sequence 60, Appl
17	472	86.0	107	15	US-10-309-762-63	Sequence 63, Appl
18	468.5	85.3	108	14	US-10-041-860-357	Sequence 357, App
19	468	85.2	234	12	US-10-292-088-24	Sequence 24, Appl
20	466	84.9	108	10	US-09-920-262A-8	Sequence 8, Appl
21	466	84.9	234	12	US-10-292-088-48	Sequence 48, Appl
22	464.5	84.6	109	9	US-09-798-058-4	Sequence 4, Appl
23	464.5	84.6	109	15	US-10-220-418-4	Sequence 4, Appl
24	464	84.5	107	12	US-10-269-711-17	Sequence 17, Appl
25	464	84.5	107	12	US-10-269-711-25	Sequence 25, Appl
26	464	84.5	107	12	US-10-269-711-29	Sequence 29, Appl
27	463	84.3	107	10	US-09-848-798-40	Sequence 40, Appl
28	463	84.3	107	12	US-10-292-088-20	Sequence 20, Appl
29	462.5	84.2	106	14	US-10-040-244-17	Sequence 17, Appl
30	462	84.2	106	16	US-10-027-725A-10	Sequence 10, Appl
31	462	84.2	108	16	US-10-408-901-20	Sequence 20, Appl
32	462	84.2	214	16	US-10-408-901-44	Sequence 44, Appl
33	461	84.0	107	12	US-10-292-088-44	Sequence 44, Appl
34	461	84.0	108	16	US-10-408-901-12	Sequence 12, Appl
35	461	84.0	132	16	US-10-469-304-23	Sequence 23, Appl
36	461	84.0	214	16	US-10-408-901-36	Sequence 36, Appl
37	460	83.8	107	12	US-09-948-939-13	Sequence 13, Appl
38	460	83.8	107	12	US-10-269-711-9	Sequence 9, Appl
39	460	83.8	107	14	US-10-269-711-13	Sequence 13, Appl
40	460	83.8	107	14	US-10-016-986-104	Sequence 104, App
41	460	83.8	108	9	US-09-056-160B-12	Sequence 12, Appl
42	460	83.8	108	11	US-09-795-798-3	Sequence 3, Appl
43	460	83.8	108	14	US-10-234-671-12	Sequence 12, Appl
44	460	83.8	109	9	US-09-811-123-6	Sequence 6, Appl
45	460	83.8	110	14	US-10-044-896-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-12
; Sequence 12, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-12

Query Match 100.0%; Score 549; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.8e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSASVGDRTVITCRASQGISWLAWYQHQPCKAPKLLIYASASSLQSGVPSRF	60
Db	1	ELTQSPSSVSASVGDRTVITCRASQGISWLAWYQHQPCKAPKLLIYASASSLQSGVPSRF	60
Qy	61	SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGQTKVEIKR	106
Db	61	SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGQTKVEIKR	106

RESULT 2

US-10-693-629-66
; Sequence 66, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:

; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 ; APPLICANT: MIKAYAMA, Toshifumi
 ; APPLICANT: YOSHIDA, Hitoshi
 ; APPLICANT: FORCE, Walker, R.
 ; APPLICANT: CHEN, Xingjie
 ; APPLICANT: TAKAHASHI, Nobuaki
 ; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
 ; FILE REFERENCE: 021286-0306473
 ; CURRENT APPLICATION NUMBER: US/10/693,629
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/13672
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US09/844,684
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: JP2001/142482
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: JP2001/310535
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: US10/040,244
 ; PRIOR FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 66
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-693-629-66

Query Match 88.2%; Score 484; DB 16; Length 223;
 Best Local Similarity 87.7%; Pred. No. 1.1e-35;
 Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 ELTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 25 QMTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYAGSLQSGVPSRF 84

 Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106
 Db 85 SGSGFGTDFLTITSLQPEDFATYCCOANSFPYTFQGTKEIKR 130

RESULT 3
 US-10-309-762-159
 ; Sequence 159, Application US/10309762
 ; Publication No. US20040018198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudas, Jean
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Handa, Masahisa
 ; APPLICANT: Gallo, Michael
 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
 ; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
 ; FILE REFERENCE: ABGENIX.027A
 ; CURRENT APPLICATION NUMBER: US/10/309,762
 ; CURRENT FILING DATE: 2002-12-02
 ; PRIOR APPLICATION NUMBER: 60/337275
 ; PRIOR FILING DATE: 2001-12-03
 ; NUMBER OF SEQ ID NOS: 246
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-309-762-159

Query Match 87.8%; Score 482; DB 15; Length 107;
 Best Local Similarity 88.6%; Pred. No. 8e-36;
 Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

 Qy 1 ELTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYAGSLQSGVPSRF 62

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIK 105
 Db 63 SGSGSGTDFLTITSLQPEDFATYCCOANSFPYTFQGTKEIK 107

 RESULT 4
 US-10-292-088-105
 ; Sequence 105, Application US/10292088
 ; Publication No. US20030211100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADUE, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI
 ; APPLICANT: FENG, XIAO
 ; TITLE OF INVENTION: ANTIBODIES TO CD40
 ; FILE REFERENCE: ABX-PF/3 US
 ; CURRENT APPLICATION NUMBER: US/10/292,088
 ; CURRENT FILING DATE: 2003-03-14
 ; PRIOR APPLICATION NUMBER: 60/348,980
 ; PRIOR FILING DATE: 2001-11-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 105
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-292-088-105

Query Match 87.6%; Score 481; DB 12; Length 107;
 Best Local Similarity 89.5%; Pred. No. 9.8e-36;
 Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 ELTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYAAASSLSQGVPSRF 62

 Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIK 105
 Db 63 SGSGSGTDFLTITSLQPEDFATYCCOANSFPYTFQGTKEIK 107

RESULT 5
 US-10-309-762-62
 ; Sequence 62, Application US/10309762
 ; Publication No. US20040018198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudas, Jean
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Handa, Masahisa
 ; APPLICANT: Gallo, Michael
 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
 ; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
 ; FILE REFERENCE: ABGENIX.027A
 ; CURRENT APPLICATION NUMBER: US/10/309,762
 ; CURRENT FILING DATE: 2002-12-02
 ; PRIOR APPLICATION NUMBER: 60/337275
 ; PRIOR FILING DATE: 2001-12-03
 ; NUMBER OF SEQ ID NOS: 246
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 62
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-309-762-62

Query Match 87.2%; Score 479; DB 15; Length 107;
 Best Local Similarity 88.6%; Pred. No. 1.5e-35;
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 ELTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHOPGKAPKLLIYAAASSLSQGVPSRF 62

QY	61	SSGSGTDFSLTISSLQLPDSATYYCOANSPPYFGGTVK 105
		: : : : : : : :
Db	63	SSGSGTDFSLTISSLQLPDSFATYYCOANSPFLFGEGTKVDIK 107

RESULT 6

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US-10-309-762-164
; Sequence 164, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-164

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Query Match      87.2%; Score 479; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-35;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
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QY 1 ELTQSPPSSVASVGDRVTITCRASQGISSWLAHYQHOPGKAPKLIIYVSAASLQSGVPSRF 60
: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 QMTQSPPSSVASVGDRVTITCRASQGISSWLAHYCQKPGKAPKLIIYAASLQSGVPSRF 62

QY 61 SGSGGYTDFTSLTISLQSPEDSANYVCQAANSFPYTFGGTKVEIK 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 SGSGSGDTFLTITSLLQPEFANFYCOAANSFFLTFGFKVDIK 107
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7

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US-10-309-762-61
; Sequence 61, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX-027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-61

Query Match      87.1%; Score 478; DB 15; Length 107;
Best Local Similarity 87.6%; Pred. No. 1.8e-35;
Matches          92; Conservative    8; Mismatches   5; Indels     0; Gaps      0;

QY      1 ELTQSPSSVSASVGDRTVTTCRASQGTSSNLAWYQHOPGKAPKLIIYSASLSQGVPSEF 60

```

Db 3 QMTQPSVSVASGVDRVITCRASQGISSWLAWFOQKFGKAPKLLIYAASSIQGVPSRF 62

Qy 61 SSGSGYTDFTLSITSIQFEDSATYYCOOANFPYTFGGTKVEIK 105

Db 63 SSGSGSTDFTLSITSIQFEDSATYYCOOANFPYTFGGTKLEIK 107

RESULT 8

```

RES001 8
US-10-309-762-64
; Sequence 64, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Folcz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ IDS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 107
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-309-762-64

```

	Query Match	87.1%	Score 478;	DB 15;	Length 107;	
	Best Local Similarity	87.6%;	Pred. No. 1.8e-35;			
	Matches 92;	Conservative	8;	Mismatches 5;	Indels 0; Gaps 0;	
QY	1	ELTQSPSSVSASVGDVRTITCRASQGISSWLAWYQHQP	GP	KAPKLLIY	SASSLSQSGVPSRF 60	
		:::::		:::::		
Db	3	QMTQSPSSVSASVGDVRTITCRASQGISSWLAWFQ	QK	GP	KAPKLLIY	SASSLSQSGVPSRF 62
		:::::		:::::		
QY	61	SGSGGYGTFSLTSSIQFDSATYYCQ	QANSFPYTFQ	GKT	VEIK 105	
		:::::		:::::		
Db	63	SGSGSGDTPLTSSLPEDPATYYCQ	ANSFPYTFQ	G	TRLEIK 107	
		:::::		:::::		

6 JUL 1964

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US-09-880-748-1881
; Sequence 1881, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1881

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Best Local Similarity 88.6%; Pred. No. 4.1e-35;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSRFS 61
Db 140 MTQSPSTLSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSRFS 199

Qy 62 GSGYGTDFSLTITSSLOQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 200 GSGSGTDFTLTITSSLOQFEDPATYCCQANSFPPLTFGGTKVEIKR 244

RESULT 10
US-10-293-418-1881
; Sequence 1881, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-293-418-1881

Query Match 87.1%; Score 478; DB 12; Length 244;
Best Local Similarity 88.6%; Pred. No. 4.1e-35;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSRFS 61
Db 140 MTQSPSTLSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSRFS 199

Qy 62 GSGYGTDFSLTITSSLOQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 200 GSGSGTDFTLTITSSLOQFEDPATYCCQANSFPPLTFGGTKVEIKR 244

RESULT 11
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 86.5%; Score 475; DB 9; Length 236;
Best Local Similarity 88.7%; Pred. No. 7.4e-35;
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSR 60
Db 25 QMTQSPSSVSASVGDRTVITCRASQGISRLWAWYQKPGKAPKLLIYVASSLQSGVPSR 84
Qy 61 GSGYGTDFSLTITSSLOQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 85 GSGSGTDFTLTITSSLOQFEDPATYCCQANSFPWTFGGTKVEIKR 130

RESULT 12
US-10-041-860-43
; Sequence 43, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-43

Query Match 86.3%; Score 474; DB 14; Length 107;
Best Local Similarity 87.6%; Pred. No. 4.2e-35;
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPCKAPKLLIYASLSQSGVPSR 60
Db 3 QMTQSPSSVSASVGDRTVITCRASQGISLWAWYQKPGKAPKLLIYVASSLQSGVPSR 62

Qy 61 GSGYGTDFSLTITSSLOQFEDSATYCCQANSFPYTFGGTKVEIK 105
Db 63 GSGSGTDFTLTITSSLOQFEDPATYCCQANSFPRTFGGTKVEIK 107

RESULT 13
US-10-041-860-218
; Sequence 218, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds
(without alignments)
431.306 Million cell updates/sec

Title: US-10-027-725A-12
Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDRTVTIT.....QQANSFFYTFGGTKVETIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/2/iaa/6C COMB.pdp.*
- 6: /cgn2_6/ptodata/2/iaa/6D COMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	94.4	233	3	US-08-812-586-45
2	518	94.4	233	4	US-09-535-832A-42
3	466	84.9	109	2	US-07-934-373C-3
4	466	84.9	109	3	US-08-437-642B-3
5	466	84.9	109	4	US-08-146-206C-3
6	466	84.9	109	4	US-09-705-686-3
7	466	84.9	109	5	US-09-705-686-3
8	463	84.3	107	3	US-09-240-274-40
9	460	83.8	107	1	US-08-276-852-104
10	460	83.8	107	1	US-08-899-575-104
11	460	83.8	107	1	US-08-899-575-104
12	460	83.8	107	5	US-09-535-832A-42
13	460	83.8	108	3	US-08-974-899-3
14	459	83.6	128	1	US-08-259-372A-14
15	459	83.6	128	1	US-08-468-671-14
16	457	83.2	107	1	US-08-276-852-84
17	457	83.2	107	1	US-08-899-575-84
18	457	83.2	107	1	US-08-899-575-84
19	457	83.2	107	3	US-09-240-274-175
20	457	83.2	107	3	US-09-240-274-175
21	457	83.2	107	5	US-09-535-832A-42
22	456	83.1	107	3	US-09-240-274-156
23	456	83.1	109	3	US-09-157-370-3
24	455	82.9	107	2	US-07-934-373C-18
25	455	82.9	107	3	US-08-437-642B-18
26	455	82.9	107	4	US-08-146-206C-18
27	455	82.9	107	4	US-09-648-067A-14

28	455	82.9	107	4	US-09-705-686-18	Sequence 18, Appl
29	455	82.9	107	5	PCT-US93-07832-18	Sequence 18, Appl
30	454	82.7	109	4	US-09-025-769B-28	Sequence 28, Appl
31	454	82.7	109	4	US-09-025-769B-43	Sequence 43, Appl
32	453	82.5	108	2	US-08-652-816A-4	Sequence 4, Appl
33	452	82.3	107	1	US-08-276-852-105	Sequence 105, App
34	452	82.3	107	1	US-08-899-575-105	Sequence 105, App
35	452	82.3	107	1	PCT-US95-08743-105	Sequence 105, App
36	452	82.3	107	5	PCT-US95-08743-105	Sequence 105, App
37	451	82.1	107	3	US-09-240-274-179	Sequence 179, App
38	450	82.0	107	3	US-08-599-226-1	Sequence 1, Appl
39	450	82.0	107	3	US-09-125-098-1	Sequence 1, Appl
40	450	82.0	107	4	US-09-540-018-1	Sequence 32, Appl
41	449.5	81.9	108	3	US-09-240-274-32	Sequence 82, Appl
42	449.5	81.9	108	3	US-09-240-274-43	Sequence 43, Appl
43	449	81.8	107	1	US-08-276-852-82	Sequence 82, Appl
44	449	81.8	107	1	US-08-899-575-82	Sequence 82, Appl
45	449	81.8	107	1	US-08-899-575-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-08-812-586-45
; Sequence 45, Application US/08812586
; Patent No. 6048704

; GENERAL INFORMATION:

; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 233 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-812-586-45

Query Match 94.4%; Score 518; DB 3; Length 233;

Best Local Similarity 96.2%; Pred. No. 3e-41;

Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVTITCRASQGSWLAHYOHQPGKAPKLLIYSASSISQSGVPSRF 60

DB 23 ELTQSPSSVSASVGDRTVTITCRASQGSWLAHYOHQPGKAPKLLIYSASSISQSGVPSRF 82

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QY 61 SGGSGYGFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 SGGSGGTDLSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 2
US-09-535-832A-42
; Sequence 42, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 4; Length 233;
Best Local Similarity 96.2%; Pred. No. 3e-41; 3; Indels 0; Gaps 0;
Matches 102; Conservative 1; Mismatches 1;

QY 1 ELTQSPSSVASVGDRVTITCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 23 ELTQSPSSVASVGDRVTITCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 82

QY 61 SGGSGYGFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 SGGSGGTDLSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 3
US-09-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

QY 61 SGGSGYGFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 SGGSGGTDLSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 108

RESULT 4
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRVTITCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRVTITCRASQDVSSYLAWYQKPKAPKLLIYVAASSLSGVSF 62

QY 61 SGGSGYGFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGGSGGTDLSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 108
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Query Match      84.9%; Score 466; DB 3; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTSSLOPDSATYYCOQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFLTSSLOPDSATYYCOQNSLPYTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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```

RESULT 5
US-08-146-206C-3
; Sequence 3, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-3

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```

Query Match      84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTSSLOPDSATYYCOQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFLTSSLOPDSATYYCOQNSLPYTFGQGTKEIKR 108
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RESULT 6
US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055

```

```

; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3

Query Match      84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFSLTSSLOPDSATYYCOQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFLTSSLOPDSATYYCOQNSLPYTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
PCR-US93-07832-3
; Sequence 3, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

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;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-3

Query Match 84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDVRVTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDVRVTITCRASQDVSSYLAHYQQKPKAPKLLIYAAASSLSQSGVPSRF 62
QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106
DB 63 SGSGGTDFTLTISSLPEDFATYCCQYNSLPYTFGGTKVEIKR 108

RESULT 8
US-09-240-274-40
; Sequence 40, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-40

Query Match 84.3%; Score 463; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.8e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDVRVTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVRVTITCRASQISSYLAHYQQKPKAPKLLIYAAASSLSQSGVPSRF 61

QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106
DB 62 SGSGGTDFTLTISSLPEDFATYCCQYNSLPYTFGGTKVEIKR 107
RESULT 9
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104
Query Match 83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDVRVTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVRVTITCRASQISSYLAHYQQKPKAPKLLIYAAASSLSQSGVPSRF 60
QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106
DB 61 SGSGGTDFTLTISSLPEDFATYCCQYNSLPYTFGGTKVEIKR 106
RESULT 10
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440

```
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVRTITCRASQGISWLAHYQHOPGKAPKLLIYASASLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDVRTITCRASQGISWLAHYQHOPGKAPKLLIYASASLSQSGVPSRF 60

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGQTKVEIKR 106
Db 61 SGSGSGTDFLTITSSLPQDFATYCCQSYSTPYTFQGQTKLEIKR 106

RESULT 11
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVRTITCRASQGISWLAHYQHOPGKAPKLLIYASASLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDVRTITCRASQGISWLAHYQHOPGKAPKLLIYASASLSQSGVPSRF 60

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGQTKVEIKR 106
Db 61 SGSGSGTDFLTITSSLPQDFATYCCQSYSTPYTFQGQTKLEIKR 106

RESULT 12
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
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SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-08743-104

Query Match 83.8%; Score 460; DB 5; Length 107;
 Best Local Similarity 85.8%; Pred. No. 3.5e-36;
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 60
 DB 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 60

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 DB 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106

RESULT 13

US-08-974-899-3
 Sequence 3, Application US/08974899
 Patent No. 6037454

GENERAL INFORMATION:
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,899
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/031971
 FILING DATE: 11/27/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-974-899-3
 Query Match 83.8%; Score 460; DB 3; Length 108;
 Best Local Similarity 84.0%; Pred. No. 3.5e-36;
 Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 62

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 DB 63 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 108

RESULT 14

US-08-259-372A-14
 Sequence 14, Application US/08259372A
 Patent No. 5565354

GENERAL INFORMATION:
 APPLICANT: Ostberg, Lars G.
 TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/259,372A
 FILING DATE: 14-JUN-1994
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/871,426
 FILING DATE: 21-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/676,036
 FILING DATE: 27-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/538,796
 FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/192,754
 FILING DATE: 11-MAY-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/925,196
 FILING DATE: 31-OCT-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/904,517
 FILING DATE: 05-SEP-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-50-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-259-372A-14

Query Match 83.8%; Score 459; DB 1; Length 128;
 Best Local Similarity 82.1%; Pred. No. 5.2e-36;
 Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 60
 DB 23 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKPKLLIYASLSQSGVPSRF 82

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
 DB 83 IGSGSGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 128

Search completed: August 8, 2004, 12:20:25
Job time : 12.6879 secs

RESULT 15
 US-08-468-671-14
 ; Sequence 14, Application US/08458671
 ; Patent No. 5648077
 ; GENERAL INFORMATION:
 ; APPLICANT: Ostberg, Lars G.
 ; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/468,671
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/259,372
 ; FILING DATE: 14-JUN-1994
 ; APPLICATION NUMBER: US 07/871,426
 ; FILING DATE: 21-APR-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/676,036
 ; FILING DATE: 27-MAR-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/538,796
 ; FILING DATE: 15-JUN-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/192,754
 ; FILING DATE: 11-MAY-1988
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/925,196
 ; FILING DATE: 31-OCT-1986
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/904,517
 ; FILING DATE: 05-SEP-1986
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-50-7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 128 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-468-671-14

Query Match	83.6%;	Score 459;	DB 1;	Length 128;
Best Local Similarity	82.1%;	Pred. No. 5.2e-36;		
Matches	87;	Conservative 11;	Mismatches 8;	Indels 0;
QY	1	ELTQSPSSVSASVGDRTVTTCTRASQGISSLWAWYQHQP	GKAPKLLIYSASSLSQSGVPSRF	60
Db	23	QMTQSPSSVSASVGDRTVTTCTRASQGISSLWAWYQKPGKAPKLLIHAASSLSQSGVPSRF	82	
QY	61	SGSGYGTDFSLTSLISLQFEDSANVYCCQANSFYTFQGTQVKVIR	106	
Db	83	IGSGSGTDFTLTSLISLQAEFANVYCCQADSLPFTFGGTVKDFKR	128	

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